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PATENT & TRADEMARK OFFICE

TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims priority under 35 U.S.C. §119(e) of U.S. Provisional Application No. 60/415,758 filed October 2, 2002, the disclosure of which application is incorporated herein by reference in its entirety.

INCORPORATION OF SEQUENCE LISTING

Two copies of the sequence listing (Copy 1 and Copy 2) and a computer readable form (CRF) of the sequence listing, all on CD-ROMs, each containing the file named Pa_00611.rpt, which is 90,549,610 bytes (measured in MS-WINDOWS) and was created on September 30, 2003, are herein incorporated by reference.

INCORPORATION OF TABLES

Table 1 which is submitted in two copies on CD-ROM, each containing the file named "Table 1.txt", which is 364 KB (measured in MS-WINDOWS) and which was created on October 25, 2006, is incorporated herein by reference.

FIELD OF THE INVENTION

Disclosed herein are seeds from transgenic plants, wherein the genome of said seed comprises recombinant polynucleotides, the expression of which results in the production of transgenic plants with enhanced phenotypes.

BACKGROUND OF THE INVENTION

Transgenic plants with improved agronomic traits such as yield, pest resistance, herbicide tolerance, improved seed compositions, and the like are desired by both farmers and consumers. Although considerable efforts in plant breeding have provided significant gains in desired phenotypes, the ability to introduce specific DNA into plant genomes provides further opportunities for generation of plants with improved and/or unique phenotypes. The ability to develop transgenic plants with improved traits depends in part on the identification of genes that are useful in recombinant DNA constructs for production of transformed plants with improved properties.

SUMMARY OF THE INVENTION

The present invention is directed to seed from a transgenic plant line, wherein said seed comprises in its genome a recombinant polynucleotide providing for expression or suppression of a polypeptide provided herein. Of particular interest is seed from a transgenic plant line, wherein said seed may be grown to produce plants having increased yield as compared to the yield of a control plant. Increased yield may be characterized as plant yield increase under non-stress conditions, or by plant yield increase under one or more environmental stress conditions. The invention also provides transgenic seed for plant lines having other enhanced phenotypes, such as enhanced plant morphology, plant physiology or seed component phenotype as compared to a corresponding phenotype of a control plant line. Of particular interest in the present invention is seed from transgenic crop plants, preferably maize (corn – *Zea mays*) or soybean (soy – *Glycine max*) plants. Other plants of interest in the present invention for production of transgenic seed that can be grown to provide plants having enhanced properties include, without limitation, cotton, canola, wheat, sunflower, sorghum, alfalfa, barley, millet, rice, tobacco, fruit and vegetable crops, and turfgrass.

In one aspect, this invention relates to the generation of transgenic plants by transformation with recombinant polynucleotides, and the identification of transgenic plants comprising such recombinant polynucleotides and having enhanced phenotypes. Of particular interest are transgenic plants that exhibit an improvement in a plant trait that is a component of yield. This aspect of the invention employs recombinant polynucleotides for expression of polypeptides that are useful for imparting desired traits to the transformed plants and recombinant polynucleotides for expression of homologs of such polypeptides as described herein. Exemplary polynucleotides which encode polypeptides of interest in the present invention are provided as SEQ ID NO:1 through SEQ ID NO:614. Sequences of the polypeptides of interest are provided as SEQ ID NO:615 through SEQ ID NO:1228, and sequences of exemplary homolog polypeptides are provided as SEQ ID NO1229 through SEQ ID NO: 27373. Tables 1-3 identifying the sequences of the present invention and their homologs are provided on the CD-ROM filed herewith.

Also of interest are recombinant polynucleotides that provide for suppression of expression of a target gene in a transgenic plant host using gene suppression methods, such as antisense or RNAi. Any of the polynucleotides provided herein as SEQ ID NO:1 through SEQ ID NO:614 may be used in such recombinant polynucleotides for gene suppression. Of particular interest are recombinant polynucleotides for gene suppression, wherein said polynucleotide targets gene suppression of the wilt-1256 protein having SEQ ID NO:853.

Thus, the present invention also comprises recombinant polynucleotides. Recombinant polynucleotides exemplified herein comprise a promoter functional in a plant cell operably joined to a DNA segment comprising encoding sequence for a polypeptide provided herein, or a homolog thereof. Such molecules are useful for production of transgenic plants having at least one improved property as the result of expression of a polypeptide of this invention or suppression of expression of a polypeptide described herein.

Also considered in the present invention is a method of producing a plant having an improved property, wherein the method comprises transforming a plant with a recombinant polynucleotide providing for expression or suppression of a polypeptide provided herein, and growing said transformed plant. In one aspect, the recombinant polynucleotide comprises a promoter functional in a plant cell operably joined to a DNA segment comprising encoding sequence for a polypeptide provided herein. The polynucleotide may be oriented with respect to the promoter to provide for transcription of sense or antisense RNA, or a combination of sense and antisense RNA, such as for use in RNAi methods of gene suppression. Of particular interest are uses of such methods to generate transgenic crop plants having increased yield.

Another aspect of the invention provides fragments of the polynucleotides of the present invention for use, for example as probes or molecular markers. Such fragments comprise at least 15 consecutive nucleotides in a sequence selected from the group consisting of SEQ ID NO:1 through SEQ ID NO:614 and complements thereof. Polynucleotide fragments of the present invention are useful as primers for PCR amplification and in hybridization assays such as transcription profiling assays, marker assays, or crop identity assays, including, for example, high throughput assays where the oligonucleotides are present in high density on a substrate, such as for example in microarrays.

DETAILED DESCRIPTION OF THE INVENTION

The present invention is directed to seed from a transgenic plant, wherein the genome of said seed comprises an exogenous polynucleotide comprising a functional portion of an encoding region for a polypeptide provided herein, and wherein plants grown from said seed exhibit an enhanced phenotype as compared to the phenotype of a control plant. Of particular interest are plants wherein the enhanced phenotype is increased yield. Exogenous polynucleotides of the present invention include recombinant polynucleotides providing for expression of mRNA encoding a polypeptide, and recombinant polynucleotides providing for expression of mRNA complementary to at least a portion of an mRNA native to the target plant for use in gene suppression.

As used herein, a "transgenic plant" is one whose genome has been altered by the incorporation of exogenous genetic material, e.g. by transformation as described herein. The term "transgenic plant" is used to refer to the plant produced from an original transformation event, or progeny from later generations or crosses of a plant so transformed, so long as the progeny contains the exogenous genetic material in its genome. By "exogenous" is meant that a nucleic acid molecule, for example, a recombinant polynucleotide, originates from outside the plant into which it is introduced. An exogenous nucleic acid molecule may comprise naturally or non-naturally occurring polynucleotides, and may be derived from the same or a different plant species than that into which it is introduced.

"Recombinant polynucleotide" refers in the present invention to a polynucleotide having a genetically engineered modification introduced through manipulation via mutagenesis, restriction enzymes, and the like. Recombinant polynucleotides may comprise DNA segments obtained from different sources, or DNA segments obtained from the same source, but which have been manipulated to join DNA segments which do not naturally exist in the joined form. A recombinant polynucleotide may exist outside of the cell, for example as a PCR fragment, or integrated into a genome, such as a plant genome.

As used herein, a "functional portion" of an encoding region for a polypeptide provided herein is a sufficient portion of the encoding region to provide the desired activity. Where expression of protein is desired, a functional portion will generally comprise the entire coding region for the polypeptide, although certain deletions, truncations, rearrangements and the like of the polypeptide may also maintain, or in some cases improve, the desired activity. One skilled in the art is aware of methods to screen for such desired modifications and such polypeptides are considered within the scope of the present invention. Where gene suppression methods are employed, smaller portions of the encoding region may be used to produce the desired effect.

"Enhanced phenotype" as used herein refers to a measurable improvement in a crop trait including, but not limited to, yield increase, including increased yield under non-stress conditions and increased yield under environmental stress conditions. Stress conditions may include, for example, drought, shade, fungal disease, viral disease, bacterial disease, insect infestation, nematode infestation, cold temperature exposure, heat exposure, osmotic stress, reduced nitrogen nutrient availability, reduced phosphorus nutrient availability and high plant density. Many agronomic traits can affect "yield", including without limitation, plant height, pod number, pod position on the plant, number of internodes, incidence of pod shatter, grain size, efficiency of nodulation and nitrogen fixation, efficiency of nutrient assimilation, resistance to biotic and abiotic stress, carbon assimilation, plant architecture, resistance to lodging, percent seed germination, seedling vigor, and juvenile traits. Other traits that can affect yield include, efficiency of germination (including germination in stressed conditions), growth rate (including growth rate in stressed conditions), ear number, seed number per ear, seed size, composition of seed (starch, oil, protein) and characteristics of seed fill.

Also of interest is the generation of transgenic plants that demonstrate enhanced phenotypic properties that may or may not confer an increase in overall plant yield. Such properties include enhanced plant morphology, plant physiology or enhanced components of the mature seed harvested from the transgenic plant. Of particular interest are enhancements in seed oil, tocopherol, protein and starch components, including increases in the quantity of any of these components, alterations in the ratios of any of these components, or production of new types of these components that do not exist in the seed from control plants. By way of example, increases in total tocopherol content are desirable, as are increases in the relative percentage of α-tocopherol produced by plants.

A "control plant" as used in the present invention is a plant used to compare against a transgenic plant grown from transgenic seed provided herein, to identify an enhanced phenotype in said transgenic plant. A suitable control plant may be a non-transgenic plant of the parental line used to generate a transgenic plant herein. A control plant may in some cases be a transgenic plant line that comprises an empty vector or marker gene, but does not contain the recombinant polynucleotide of the present invention that is expressed in the transgenic plant being evaluated. In general, a control plant is a plant of the same line or variety as the transgenic plant being tested.

"Increased yield" of a transgenic plant of the present invention may be evidenced and measured in a number of ways, including test weight, seed number per plant, seed weight, seed number per unit area (i.e. seeds, or weight of seeds, per acre), bushels per acre, tonnes per acre, tons per acre, kilo per hectare. For example, maize yield may be measured as production of shelled corn kernels per unit of production area, e.g. in bushels per acre or metric tons per hectare, often reported on a moisture adjusted basis, e.g. at 15.5 % moisture. Increased yield may result from improved utilization of key biochemical compounds, such as nitrogen, phosphorous and carbohydrate, or from improved responses to environmental stresses, such as cold, heat, drought, salt, and attack by pests or pathogens. Polynucleotides of the present invention may also be used to provide plants having improved growth and development, and ultimately increased yield, as the result of modified expression of plant growth regulators or modification of cell cycle or photosynthesis pathways.

"Expression" as used herein refers to transcription of DNA to produce RNA. The resulting RNA may be without limitation mRNA encoding a protein, antisense RNA that is complementary to an mRNA encoding a protein, or an RNA transcript comprising a combination of sense and antisense gene regions, such as for use in RNAi technology. Expression as used herein may also refer to production of encoded protein from mRNA.

"Gene suppression" is used herein to refer to reduction or suppression of expression of a target protein in a host cell as the result of transcription of a recombinant polynucleotide provided herein, wherein the polynucleotide is oriented with respect to a promoter to provide for production of RNA having a gene silencing effect, such as antisense RNA or interfering RNA (RNAi).

Transgenic Plants and Seed

Transgenic plant seed provided by this invention may be grown to generate transgenic plants having an enhanced phenotype as compared to an appropriate control line. Such seed is obtained by screening transformed plants for enhanced phenotype resulting from the introduction of a recombinant polynucleotide into the genomic DNA of tissue from a parental line. The recombinant polynucleotide is introduced into the genome in sufficient quantity to produce transgenic cells that can be cultured into transgenic plants having an enhanced phenotype as compared to the parental line or other appropriate control. Such transgenic cells are cultured into transgenic plants that produce progeny transgenic seed. Preferably, the screening program is designed to evaluate multiple transgenic plants (events) comprising the recombinant polynucleotides being evaluated, e.g. from 2 to 20 or more transgenic events. Although the design of a recombinant polynucleotide is based on a rational expectation of a phenotypic modification, the present invention also contemplates that unexpected, yet desired enhanced phenotypes may be obtained.

Transgenic plants grown from transgenic seed provided herein demonstrate improved phenotypes that contribute to increased yield or other increased plant value, including, for example, improved seed quality. Of particular interest are plants having enhanced plant growth and development, stress tolerance, seed development, light response, flower development, and carbon and/or nitrogen metabolism properties.

Plant growth and development enhancements may be obtained, for example, by modification of cell cycle pathways, purine biosynthesis, adenylate transport, steroid biosynthesis and signaling, protein degradation, programmed cell death, and by modification of activity of key plant development components, such as receptor kinases, elongation factors, growth regulators, cytokinins and various transcription factors.

Stress tolerance enhancements may be obtained, for example by modification of glycine betaine biosynthesis, transcription factor activity, phospholipid signaling, osmosensitivity, oxidative stress tolerance, disease resistance, abscisic acid biosynthesis or signaling, 14-3-3 protein activity, and flavonoid biosynthesis, and modification of expression of proteins such as nonsymbiotic hemoglobins, LEA-like proteins, freezing associated proteins or wilt related proteins.

Seed development enhancements may be obtained, for example by modification of expression of kernel expressed transcription factors, such as provided as SEQ ID NO:477 through SEQ ID NO:522, or transcription factors associated with high oil corn (SEQ ID NO:554 and SEQ ID NO:555), modification of nitrate transport, and modification of S-domain receptor like protein kinases associated with aleurone development.

Light response enhancements may be obtained, for example by modification of expression of PhyA regulated genes such as provided as SEQ ID NO:195 through SEQ ID NO:217, or modification of expression of phytochrome or microbial phytochrome like proteins.

Flower development enhancements may be obtained, for example by modification of expression of genes related to flowering time such as provided herein as SEQ ID NO: 131, SEQ ID NO:132, SEQ ID NO: 134 through SEQ ID NO: 139, SEQ ID NO:153 through SEQ ID NO:155, SEQ ID NO:158 through SEQ ID NO:162, SEQ ID NO:529, and by modification of expression of casein kinase.

Carbon/nitrogen metabolism enhancements may be obtained, for example by modification of sucrose transport, starch biosynthesis, nitrogen sensing, including for example, by modification of expression of DUF6 transporters, PPDK, or starch biosynthesis genes, such as SBPase (sedoheptulose-1,7-bisphosphatase), SPS (sucrose phosphate synthase) and SPP (sucrose phosphate phosphatase).

Polypeptides useful for generation of transgenic plants having enhanced properties are provided in Table 4 below and as SEQ ID NO:615 through SEQ ID NO:1228.

"PEP SEQ ID NO" refers to a particular amino acid sequence in the Sequence Listing

"PHE ID" refers to an arbitrary number used to identify a particular recombinant polynucleotide corresponding to the translated protein encoded by the polynucleotide.

"NUC SEQ ID NO" refers to a particular nucleic acid sequence in the Sequence Listing which defines a polynucleotide used in a recombinant polynucleotide of this invention.

"GENE NAME" refers to a common name for the recombinant polynucleotide.

"GENE EFFECT" refers to the effect of the expressed polypeptide in providing yield improvement or other enhanced property

"CODING SEQUENCE" referS to peptide coding segments of the polynucleotide.

"SPECIES" refers to the organism from which the polynucleotide DNA was derived.

TABLE 4

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
615	PHE0000002	1	Arabidopsis AtHAP3a	Stress tolerance	103-525	Arabidopsis thaliana
616	PHE0000003	2	corn AtHAP3a -like1	Stress tolerance	149-817	Zea mays
617	PHE0000004	3	corn AtHAP3a -like2	Stress tolerance	196-750	Zea mays
618	PHE0000005	4	corn AtHAP3a -like3	Stress tolerance	91-588	Zea mays
619	PHE0000021	5	Arabidopsis CCA1	Stress tolerance	238-2061	Arabidopsis thaliana
620	PHE0000041	6	corn hemoglobin 2	Stress tolerance	67-639	Zea mays
621	PHE0000066	7	At TOR1-like	Stress tolerance	1462-1626, 1850-2188, 2267-2341, 2519-2691, 3060-3158, 3442-3634, 3703-3846, 3984-4153, 4233-4437, 4511-4699, 4907-5059, 5528-5649, 5735-5837, 5912-6007, 6309-6439, 7148-7250, 7326-7508, 7583-7675, 7914-8012, 8096-8194, 8247-8451, 8764-8888, 8999-9051, 9493-9616, 9734-9904, 10380-10532, 10599-10751, 11235-11306, 11414-11548, 11625-11686, 11819-11916, 12172-12281, 12358-12531, 12647-12712, 13059-13127, 13235-13345, 13685-13825, 13917-14045, 14168-14333, 14421-14629, 14795-15001, 15165-15278, 15383-15613, 15896-15976, 16081-16155, 16234-16300, 16400-16560, 16707-16880, 16967-17095, 17187-17270, 17379-17440, 17521-17593, 17678-18001, 18086-18385	Arabidopsis thaliana
622	PHE0000078	8	E. coli glnB	Carbon and/or nitrogen metabolism	35-373	Escherichia coli
623	PHE0000080	9	G28/BAA32418	Stress tolerance	3-803	Arabidopsis thaliana
624	PHE0000081	10	G378	Stress tolerance	1-723	Arabidopsis thaliana
625	PHE0000094	11	G464	Stress tolerance	41-661	Arabidopsis thaliana
626	PHE0000112	12	Curly Leaf - variant 1	Apomixis	108-901, 1084-1177, 1251-3055	Zea mays

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
627	PHE0000113	13	Curly Leaf - variant 2	Apomixis	113-912, 1083-1191, 1257-2806	Zea mays
628	PHE0000140	14	casein kinase II alpha subunit	Flower development	202-1200	Zea mays
629	PHE0000151	15	Adenosylhomo cysteinase	Stress tolerance	71-1525	Zea mays
630	PHE0000199	16	ethylene response sensor	Ethylene signaling	79-1986	Zea mays
631	PHE0000214	17	maize glycine rich protein	Stress tolerance	70-540	Zea mays
632	PHE0000364	18	wilt-like 1	Stress tolerance	316-1644	Zea mays
633	PHE0000365	19	wilt-like 2	Stress tolerance	334-1512	Zea mays
634	PHE0000366	20	wilt-like 3	Stress tolerance	263-1552	Zea mays
635	PHE0000367	21	wilt-like 4	Stress tolerance	202-1419	Zea mays
636	PHE0000373	23	G1411	Plant growth and development	1-747	Arabidopsis thaliana
637	PHE0000374	24	G1449	Plant growth and development	1-474	Arabidopsis thaliana
638	PHE0000375	25	G1635	Plant growth and development	1-1161	Arabidopsis thaliana
639	PHE0000376	26	G188	Stress tolerance	1-1044	Arabidopsis thaliana
640	PHE0000377	27	G19	Stress tolerance	1-747	Arabidopsis thaliana
641	PHE0000378	28	G559	Plant growth and development	1-1194	Arabidopsis thaliana
642	PHE0000379	29	G865	Plant growth and development	1-636	Arabidopsis thaliana
643	PHE0000381	30	corn G214	Stress tolerance	1-2160	Zea mays
644	PHE0000383	31	700151210_FLI - corn L5 a	Plant growth and development	61-966	Zea mays
645	PHE0000384	32	LIB3957-023-C10_FLI - corn C-type cyclin	Plant growth and development	134-904	Zea mays
646	PHE0000405	33	ASH2 - F17I14_190 (Suppressor of hog1)	Stress tolerance	370-1965	Arabidopsis thaliana
647	PHE0000406	34	soy ASH2-like 1	Stress tolerance	67-1329	Glycine max
648	PHE0000407	35	soy ASH2-like 3	Stress tolerance	37-1464	Glycine max
649	PHE0000408	36	soy ASH2-like 4	Stress tolerance	49-1971	Glycine max
650	PHE0000409	37	corn pescadillo-like 1	Plant growth and development	55-1911	Zea mays
651	PHE0000410	38	yeast pescadillo homologue - Z72888	Plant growth and development	657-2474	Saccharomyces cerevisiae
652	PHE0000424	39	soy GA2-oxidase	Plant growth and development	38-1036	Glycine max
653	PHE0000447	40	corn phospholipase C 1	Stress tolerance	228-1985	Zea mays
654	PHE0000448	41	corn diacylglycerol kinase 2	Stress tolerance	141-2282	Zea mays
655	PHE0000449	42	corn Ins(1,4,5)P(3) 5-phosphatase 1	Stress tolerance	116-1849	Zea mays

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
656	PHE0000459	43	Anabaena SPP	Carbon and/or nitrogen metabolism	1-747	Nostoc PCC7120
657	PHE0000460	44	Corn SPP	Carbon and/or nitrogen metabolism	1-1269	Zea mays
658	PHE0000461	45	UDPgpp	Carbon and/or nitrogen metabolism	1-1419	Zea mays
659	PHE0000464	46	soy U-box protein 1	Plant growth and development	137-2119	Glycine max
660	PHE0000465	47	soy U-box protein 2	Plant growth and development	63-1355	Glycine max
661	PHE0000466	48	soy U-box protein 3	Plant growth and development	26-2053	Glycine max
662	PHE0000467	49	corn U-box protein 3	Plant growth and development	197-1774	Zea mays
663	PHE0000468	50	corn U-box protein 4	Plant growth and development	104-1183	Zea mays
664	PHE0000474	51	yeast ado1	Stress tolerance	567-1589	Saccharomyces cerevisiae
665	PHE0000475	52	corn adenosine kinase 1	Stress tolerance	264-1289	Zea mays
666	PHE0000476	53	soy adenosine kinase 2	Stress tolerance	90-1112	Glycine max
667	PHE0000477	54	Synechocystis hypothetical sugar kinase - BAA10827	Stress tolerance	86-1087	Synechocystis sp. PCC 6803
668	PHE0000478	55	corn adenosylhomocysteinase 1	Stress tolerance	38-1492	Zea mays
669	PHE0000479	56	yeast S-adenosyl-L-homocysteine hydrolase - NP_010961	Stress tolerance	142-1491	Saccharomyces cerevisiae
670	PHE0000480	57	Synechocystis S-adenosylhomocysteine hydrolase-BAA18079	Stress tolerance	305-1582	Synechocystis sp. PCC 6803
671	PHE0000481	58	soy RING finger protein 1 [BCRA1]	Plant growth and development	64-1494	Glycine max
672	PHE0000482	59	Aspergillus yA (laccase 1) - X52552	Stress tolerance	913-1107, 1162-1217, 1289-1459, 1535-1705, 1759-1884, 1949-3059	Emericella nidulans
673	PHE0000483	60	Synechocystis Sucrose phosphate synthase	Carbon and/or nitrogen metabolism	1-2160	Synechocystis sp. PCC 6803
674	PHE0000487	61	yeast HAL3-Z28297	Plant growth and development	64-1752	Saccharomyces cerevisiae
675	PHE0000488	62	yeast GLC8-P41818	Plant growth and development	2556-3245	Saccharomyces cerevisiae

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
676	PHE0000489	63	corn HAL3-like 1-LIB3060-046-G12_FLI	Plant growth and development	24-659	Zea mays
677	PHE0000490	64	corn HAL3-like 2-	Plant growth and development	237-881	Zea mays
678	PHE0000491	65	corn GLC8-like 2	Plant growth and development	232-726	Zea mays
679	PHE0000492	66	corn GLC8-like 1	Plant growth and development	98-625	Zea mays
680	PHE0000495	69	Agrobacterium aiiA-like protein [attM] - AAD43990	Stress tolerance	98-865	Agrobacterium tumefaciens
681	PHE0000496	70	Xylella aiiA-like protein - XF1361	Stress tolerance	365-1204	Xylella fastidiosa
682	PHE0000497	71	Xanthomonas aiiA - like protein	Stress tolerance	121-1044	
683	PHE0000498	72	corn histone H4	Seed development	83-391	Zea mays
684	PHE0000499	73	high sulfur zein protein precursor	Seed development	29-661	Zea mays
685	PHE0000500	74	corn RING finger protein 25	Plant growth and development	353-1771	Zea mays
686	PHE0000501	75	corn MKP 1 [MAP kinase 4]	Signal transduction	157-1278	Zea mays
687	PHE0000502	76	corn MKP 3 [MAP kinase 5]	Signal transduction	110-1300	Zea mays
688	PHE0000503	77	corn MKP 4	Signal transduction	76-1185	Zea mays
689	PHE0000504	78	corn MKP 6	Signal transduction	411-2174	Zea mays
690	PHE0000505	79	corn MKP 7	Signal transduction	382-1854	Zea mays
691	PHE0000506	80	corn MKP 8 [cdc2 kinase]	Signal transduction	217-1098	Zea mays
692	PHE0000507	81	soy MKP 1	Signal transduction	175-1293	Glycine max
693	PHE0000508	82	soy MKP 4	Signal transduction	334-1446	Glycine max
694	PHE0000509	83	corn ABF2-like 1	Stress tolerance	141-350,440-1315	Zea mays
695	PHE0000510	84	soy ABF2-like 1	Stress tolerance	114-1046	Glycine max
696	PHE0000511	85	maize PPDK	Carbon and/or nitrogen metabolism	131-3043	Zea mays
697	PHE0000512	86	yeast YOR161c - Z75069	Stress tolerance	1002-2621	Saccharomyces cerevisiae
698	PHE0000513	87	yeast HNM1 - Z72599	Stress tolerance	419-2110	Saccharomyces cerevisiae
699	PHE0000514	88	Xylella SAG13-like - E82748	Plant growth and development	67-843	Xylella fastidiosa

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
700	PHE0000515	89	corn SAG13-like 1	Plant growth and development	74-862	Zea mays
701	PHE0000516	90	soy SAG13-like 1	Plant growth and development	49-855	Glycine max
702	PHE0000517	91	soy SAG13-like 2	Plant growth and development	25-837	Glycine max
703	PHE0000518	92	Nostoc punctiforme SAG13-like	Plant growth and development	68-853	Nostoc punctiforme
704	PHE0000520	93	corn clavata3-like	Plant growth and development	145-384	Zea mays
705	PHE0000521	94	corn clavata3-like	Plant growth and development	22-255	Zea mays
706	PHE0000523	96	corn clv3-like 2	Plant growth and development	69-356	Zea mays
707	PHE0000525	98	corn violaxanthin de-epoxidase	Stress tolerance	77-1414	Zea mays
708	PHE0000526	99	rice serine acetyltransferase 1	Stress tolerance	51-1070	Oryza sativa
709	PHE0000527	100	rice serine acetyltranferase 2	Stress tolerance	131-1192	Oryza sativa
710	PHE0000528	101	corn CEO-like protein	Stress tolerance	134-1873	Zea mays
711	PHE0000529	102	wheat nicotianamine aminotransferase	Iron uptake	43-1041	Triticum aestivum
712	PHE0000530	103	corn nicotianamine synthase 1	Iron uptake	55-1146	Zea mays
713	PHE0000531	104	corn ys1-like1	Iron uptake	277-2292	Zea mays
714	PHE0000532	105	rice glutamate decarboxylase	Plant growth and development	77-1552	Oryza sativa
715	PHE0000533	106	rice GA2 oxidase	Plant growth and development	74-1219	Oryza sativa
716	PHE0000534	107	corn mlo-like 1	Plant growth and development	57-1583	Zea mays
717	PHE0000535	108	corn G alpha 1	Plant growth and development	220-1329	Zea mays
718	PHE0000536	109	corn G beta 2	Plant growth and development	58-1059	Zea mays
719	PHE0000537	110	corn g gamma-like 1	Plant growth and development	64-407,514-655	Zea mays
720	PHE0000538	111	rice tubby 1	Plant growth and development	4-1221	Oryza sativa
721	PHE0000539	112	maize tubby 3	Plant growth and development	49-1122	Zea mays
722	PHE0000540	113	maize tubby 4	Plant growth and development	257-1600	Zea mays
723	PHE0000541	114	corn tubby 5	Plant growth and development	100-1200	Zea mays
724	PHE0000542	115	maize tubby 6	Plant growth and development	83-1390	Zea mays

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
725	PHE0000543	116	maize tubby 7	Plant growth and development	125-1327	Zea mays
726	PHE0000544	117	corn tubby 9	Plant growth and development	333-1700	Zea mays
727	PHE0000545	118	rice LRR.F-box protein 1	Plant growth and development	83-1867	Oryza sativa
728	PHE0000546	119	corn LRR.F-box protein 7	Plant growth and development	167-1936	Zea mays
729	PHE0000547	120	cotton ttg1-1	Stress tolerance	19-1056	Gossypium hirsutum
730	PHE0000548	121	corn nucellin-like protein 1	Seed development	42-1424	Zea mays
731	PHE0000549	122	rice nucellin-like protein 1	Seed development	37-1443	Oryza sativa
732	PHE0000550	123	rice G1449-like 1	Plant growth and development	107-652	Oryza sativa
733	PHE0000551	124	rice LEA 1	Stress tolerance	87-686	Oryza sativa
734	PHE0000552	125	rice LEA 2 [wsi18]	Stress tolerance	70-714	Oryza sativa
735	PHE0000553	126	corn LEA 1	Stress tolerance	94-1008	Zea mays
736	PHE0000554	127	corn LEA 2	Stress tolerance	85-777	Zea mays
737	PHE0000555	128	corn adenylate transporter 1	Plant growth and development	49-1938	Zea mays
738	PHE0000556	129	Xylella adenylate transporter - XF1738	Plant growth and development	54-1376	Xylella fastidiosa
739	PHE0000557	130	yeast AAC2 - Z35791	Plant growth and development	66-1022	Saccharomyces cerevisiae
740	PHE0000558	131	yeast TFS1 - X62105	Flower development	16-675	Saccharomyces cerevisiae
741	PHE0000559	132	yeast YLR179C-AAB67472	Flower development	124-729	Saccharomyces cerevisiae
742	PHE0000560	133	ZmSPS2-2	Carbon and/or nitrogen metabolism	29-2920	Zea mays
743	PHE0000561	134	rice FPF1-like 1	Flower development	93-458	Oryza sativa
744	PHE0000562	135	rice FPF1-like 3	Flower development	60-413	Oryza sativa
745	PHE0000563	136	corn FPF1-like 1	Flower development	132-473	Zea mays
746	PHE0000564	137	corn FPF1-like 6	Flower development	31-345	Zea mays
747	PHE0000565	138	corn FLC-like 3	Flower development	210-905	Zea mays
748	PHE0000566	139	corn FLC-like 9	Flower development	305-976	Zea mays
749	PHE0000567	140	corn selenium-binding protein	Stress tolerance	239-1717	Zea mays
750	PHE0000568	141	maize glutathione S-transferase IV	Stress tolerance	103-771	Zea mays

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
751	PHE0000569	142	calcium-dependent protein kinase	Stress tolerance	177-1844	Zea mays
752	PHE0000570	143	protein kinase CK2 regulatory subunit CK2B3	Stress tolerance	178-993	Zea mays
753	PHE0000571	144	19K zein precursor	Stress tolerance	46-747	Zea mays
754	PHE0000572	145	corn EREBP/AP2-like transcription factor	Stress tolerance	114-1196	Zea mays
755	PHE0000573	146	G-box binding factor 1	Stress tolerance	145-1275	Zea mays
756	PHE0000574	147	corn high mobility group protein	Stress tolerance	145-615	Zea mays
757	PHE0000575	148	corn glycine-rich RNA-binding protein	Stress tolerance	70-492	Zea mays
758	PHE0000576	149	corn enolase 1	Stress tolerance	86-1423	Zea mays
759	PHE0000577	150	maize RING finger protein	Stress tolerance	72-680	Zea mays
760	PHE0000578	151	maize 60S acidic ribosomal protein P0	Stress tolerance	123-1079	Zea mays
761	PHE0000579	152	corn nucleotide-binding protein	Stress tolerance	223-1266	Zea mays
762	PHE0000580	153	MADS affecting flowering 1-AAK37527	Flower development	31-618	Arabidopsis thaliana
763	PHE0000581	154	G1760 - Q9SZJ6	Flower development	50-733	Arabidopsis thaliana
764	PHE0000582	155	G2010 - CAB56582	Flower development	1-522	Arabidopsis thaliana
765	PHE0000583	156	SAG13 - AAF09487	Plant growth and development	1-903	Arabidopsis thaliana
766	PHE0000584	157	Rice SAG13-like	Plant growth and development	7-786	Oryza sativa
767	PHE0000585	158	corn FLT-like 1	Flower development	317-835	Zea mays
768	PHE0000586	159	corn FLT-like 2	Flower development	65-595	Zea mays
769	PHE0000587	160	corn FLT-like 3	Flower development	72-263, 626-994	Zea mays
770	PHE0000588	161	rice leafy - AB005620	Flower development	76-1245	Oryza sativa
771	PHE0000589	162	corn HD1-like 1	Flower development	93-926	Zea mays
772	PHE0000590	163	rice plastidic ATP/ADP-transporter - BAB40979	Plant growth and development	109-915, 2211-2480, 2563-2706, 2792-3145, 3591-3950	Oryza sativa
773	PHE0000591	164	rice L5 a	Plant growth and development	80-991	Oryza sativa
774	PHE0000592	165	corn L5	Plant growth and development	61-966	Zea mays

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
775	PHE0000593	166	corn L5-like	Plant growth and development	8-871	Zea mays
776	PHE0000594	167	Agrobacterium ornithine decarboxylase	Plant growth and development	24-1562	Agrobacterium tumefaciens
777	PHE0000601	168	corn IAP-like RING finger protein 1	Plant growth and development	179-1291	Zea mays
778	PHE0000603	170	corn BAX inhibitor 1-like 1	Plant growth and development	157-906	Zea mays
779	PHE0000604	171	corn Bax inhibitor 1-like 2	Plant growth and development	113-697	Zea mays
780	PHE0000605	172	corn Bax inhibitor 1-like 3	Plant growth and development	144-890	Zea mays
781	PHE0000606	173	corn caspase-like 1	Plant growth and development	141-1193	Zea mays
782	PHE0000607	174	corn caspase-like 2	Plant growth and development	86-1018	Zea mays
783	PHE0000608	175	corn caspase-like 3	Plant growth and development	74-1141	Zea mays
784	PHE0000609	176	yeast YOR197w	Plant growth and development	186-1547	Saccharomyces cerevisiae
785	PHE0000610	177	soy Lls1-like	Plant growth and development	7-1695	Glycine max
786	PHE0000611	178	Synechocystis Rieske iron-sulfur protein	Plant growth and development	38-1447	Synechocystis sp. PCC 6803
787	PHE0000612	179	Arabidopsis AGL15	Plant growth and development	80-892	Arabidopsis thaliana
788	PHE0000613	180	yeast OST2	Plant growth and development	24-425	Saccharomyces cerevisiae
789	PHE0000614	181	corn DAD1	Plant growth and development	72-413	Zea mays
790	PHE0000615	182	corn pirin	Plant growth and development	98-1222	Zea mays
791	PHE0000616	183	corn betaine-aldehyde dehydrogenase	Stress tolerance	17-1531	Zea mays
792	PHE0000617	184	rice betaine aldehyde dehydrogenase	Stress tolerance	93-1610	Oryza sativa
793	PHE0000618	185	yeast PEM1/CHO2	Stress tolerance	617-3226	Saccharomyces cerevisiae
794	PHE0000619	186	yeast PEM2/OPI3	Stress tolerance	160-780	Saccharomyces cerevisiae
795	PHE0000620	187	corn phosphoethanolamine N-methyltransferase 2	Stress tolerance	392-1894	Zea mays
796	PHE0000621	188	E. coli betT	Stress tolerance	36-2069	Escherichia coli
797	PHE0000622	189	Xenorhabdus BetT-like 1	Stress tolerance	29-2068	Xenorhabdus sp.
798	PHE0000623	190	corn NHX1-like 1	Stress tolerance	38-1675	Zea mays
799	PHE0000624	191	OsNHX1 - AB021878	Stress tolerance	297-1904	Oryza sativa

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
800	PHE0000625	192	corn vacuolar H+-pyrophosphatase 1	Stress tolerance	124-2409	Zea mays
801	PHE0000626	193	corn vacuolar H+-pyrophosphatase 2	Stress tolerance	93-2390	Zea mays
802	PHE0000627	194	corn vacuolar H+-pyrophosphatase 5	Stress tolerance	35-2329	Zea mays
803	PHE0000628	195	soy homeobox-leucine zipper protein homolog h1-	Light response	66-920	Glycine max
804	PHE0000629	196	soy zinc finger protein	Light response	98-622	Glycine max
805	PHE0000630	197	soy TGACG-motif-binding protein STF2	Light response	82-1053	Glycine max
806	PHE0000631	198	corn putative zinc finger protein	Light response	225-842	Zea mays
807	PHE0000632	199	soy AP2 domain transcription factor	Light response	227-928	Glycine max
808	PHE0000633	200	soy pseudo-response regulator	Light response	27-2060	Glycine max
809	PHE0000634	201	soy CONSTANS-like B-box zinc finger protein	Light response	108-1229	Glycine max
810	PHE0000635	202	soy RPT2-like	Light response	23-1762	Glycine max
811	PHE0000636	203	corn myb-related protein	Light response	34-1101	Zea mays
812	PHE0000637	204	Arabidopsis salt-tolerance protein	Light response	274-1017	Arabidopsis thaliana
813	PHE0000638	205	soy AP2 domain transcription factor	Light response	98-1555	Glycine max
814	PHE0000639	206	soy late elongated hypocotyl	Light response	626-2875	Glycine max
815	PHE0000640	207	soy zinc finger protein	Light response	139-1416	Glycine max
816	PHE0000641	208	soy putative protein kinase	Light response	73-1764	Glycine max
817	PHE0000642	209	soy auxin-responsive GH3 protein	Light response	42-1820	Glycine max
818	PHE0000643	210	corn ripening-related protein	Light response	131-775	Zea mays
819	PHE0000644	211	corn beta-expansin 4	Light response	97-1020	Zea mays
820	PHE0000645	212	corn hypothetical protein	Light response	330-716	Zea mays
821	PHE0000646	213	corn unknown protein	Light response	69-710	Zea mays
822	PHE0000647	214	corn unknown protein	Light response	234-563	Zea mays
823	PHE0000648	215	corn unknown protein	Light response	169-1542	Zea mays
824	PHE0000649	216	soy unknown protein	Light response	585-1889	Glycine max
825	PHE0000650	217	corn unknown protein	Light response	211-2514	Zea mays
826	PHE0000651	218	rice Lls1 (CAO) - AF284781	Light response	100-1722	Oryza sativa

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
827	PHE0000654	219	G896	Plant growth and development	47-1147	Arabidopsis thaliana
828	PHE0000655	220	G1435	Plant growth and development	8-901	Arabidopsis thaliana
829	PHE0000656	221	LIB4074-003-H1_FLI - corn G1435-like	Plant growth and development	83-856	Zea mays
830	PHE0000658	222	G1496	Plant growth and development	116-1120	Arabidopsis thaliana
831	PHE0000660	223	700072387_FLI - ZmSPS3-1	Carbon and/or nitrogen metabolism	89-3265	Zea mays
832	PHE0000661	224	GATE90 - ZmSPS2-3	Carbon and/or nitrogen metabolism	72-2987	Zea mays
833	PHE0000662	225	corn ELI17-like protein 1	Disease resistance	7-1350	Zea mays
834	PHE0000663	226	soy ELI17-like protein 1	Disease resistance	63-1355	Glycine max
835	PHE0000664	227	X58872 - E. coli hmp1	Nitric oxide signaling	293-1483	Escherichia coli
836	PHE0000665	228	Nostoc sp. PCC 7120 glnB	Carbon and/or nitrogen metabolism	1074-1412	Nostoc PCC7120
837	PHE0000666	229	Brassica P-II	Carbon and/or nitrogen metabolism	49-639	Brassica napus
838	PHE0000700	230	Arabidopsis eskimo 1	Stress tolerance	592-2052	Arabidopsis thaliana
839	PHE0000701	231	soy 1-deoxy-D-xylulose-5-phosphate reductoisomerase-	Isoprenoid biosynthesis	76-1500	Glycine max
840	PHE0000702	232	Synechocystis 1-deoxy-D-xylulose-5-phosphate reductoisomerase-D64000	Isoprenoid biosynthesis	100-1284	Synechocystis sp. PCC 6803
841	PHE0000703	233	Agrobacterium 1-deoxy-D-xylulose 5-phosphate reductoisomerase-AAK88334	Isoprenoid biosynthesis	52-1245	Agrobacterium tumefaciens
842	PHE0000704	234	corn 1-deoxy-D-xylulose-5-phosphate synthase-	Isoprenoid biosynthesis	289-2445	Zea mays
843	PHE0000705	235	Agrobacterium 1-deoxy-D-xylulose-5-phosphate synthase-AAK86554	Isoprenoid biosynthesis	13-1932	Agrobacterium tumefaciens

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
844	PHE0000706	236	Xylella 1-deoxyxylulose-5-phosphate synthase-AAF85048	Isoprenoid biosynthesis	38-2050	Xylella fastidiosa
845	PHE0000709	237	corn HMT 1 (N-methyltransferase)	Stress tolerance	102-1070	Zea mays
846	PHE0000710	238	corn HMT 2 (N-methyltransferase)	Stress tolerance	94-1107	Zea mays
847	PHE0000711	239	E. coli yagD homocysteine S-methyltransferase-Q47690	Stress tolerance	21-953	Escherichia coli
848	PHE0000712	240	yeast Mht1 - NP_013038	Stress tolerance	60-1034	Saccharomyces cerevisiae
849	PHE0000713	241	corn H2A.F/Z 1	DNA integration	102-515	Zea mays
850	PHE0000714	242	corn H2A 1	DNA integration	56-457	Zea mays
851	PHE0000715	243	corn H2A 3	DNA integration	71-541	Zea mays
852	PHE0000716	244	corn H2A 7	DNA integration	33-512	Zea mays
853	PHE0000717	245	wilt-1256	Stress tolerance	316-1980	Zea mays
854	PHE0000735	246	corn NAD(P)H quinone oxidoreductase	Stress tolerance	67-834	Zea mays
855	PHE0000736	247	rice CBP80 - AY017415	Stress tolerance	76-2808	Oryza sativa
856	PHE0000737	248	yeast GCR3 - D10224	Stress tolerance	908-3484	Saccharomyces cerevisiae
857	PHE0000738	249	corn CBP20	Stress tolerance	8-736	Zea mays
858	PHE0000739	250	yeast CBC2 - Z73534	Stress tolerance	2352-2978	Saccharomyces cerevisiae
859	PHE0000740	251	rice serine decarboxylase - AAG12476	Stress tolerance	37-289, 1008-1239, 1601-1794, 1915-2048, 2422-2621, 2796-2943, 3677-3790	Oryza sativa
860	PHE0000741	252	corn serine decarboxylase	Stress tolerance	21-1376	Zea mays
861	PHE0000742	253	soy serine decarboxylase	Stress tolerance	94-1542	Glycine max
862	PHE0000743	254	yeast DBF2 - P22204	Plant growth and development	1-1716	Saccharomyces cerevisiae
863	PHE0000744	255	yeast DBF20 - P32328	Plant growth and development	1-1692	Saccharomyces cerevisiae
864	PHE0000745	256	Arabidopsis agl8 - Q38876	Plant growth and development	1-726	Arabidopsis thaliana
865	PHE0000746	257	corn AGL8-like B	Plant growth and development	1-753	Zea mays
866	PHE0000747	258	corn PHR1-like 1	Plant growth and development	150-1496	Zea mays

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
867	PHE0000748	259	corn PHR1-like 2	Plant growth and development	55-1302	Zea mays
868	PHE0000749	260	Nitrosomonas europaea dual function SBPase/FBPase-	Carbon and/or nitrogen metabolism	94-1095	Nitrosomonas europaea
869	PHE0000750	261	rice VP14-like 1	Stress tolerance	23-1936	Oryza sativa
870	PHE0000751	262	rice VP14-like 2	Stress tolerance	220-1947	Oryza sativa
871	PHE0000754	263	rice ANT-like	Flower development	1-1926	Oryza sativa
872	PHE0000755	264	Nostoc sp. PCC 7120 GlpX protein	Carbon and/or nitrogen metabolism	1-1035	Nostoc PCC7120
873	PHE0000756	265	Nostoc punctiforme strain ATCC 29133 GlpX protein-NOS1c0617	Carbon and/or nitrogen metabolism	1-1035	Nostoc punctiforme
874	PHE0000757	266	Anabaena SPS C154	Carbon and/or nitrogen metabolism	1-1275	Nostoc PCC7120
875	PHE0000758	267	Anabaena SPS C287	Carbon and/or nitrogen metabolism	1-1266	Nostoc PCC7120
876	PHE0000762	268	G557 (HY5)	Light response	1-507	Arabidopsis thaliana
877	PHE0000763	269	G189	Plant growth and development	1-951	Arabidopsis thaliana
878	PHE0000764	270	G736	Plant growth and development	1-510	Arabidopsis thaliana
879	PHE0000766	272	G671	Plant growth and development	1-1056	Arabidopsis thaliana
880	PHE0000767	273	G247	Plant growth and development	1-660	Arabidopsis thaliana
881	PHE0000768	274	G1384	Plant growth and development	1-942	Arabidopsis thaliana
882	PHE0000769	275	G779	Plant growth and development	1-594	Arabidopsis thaliana
883	PHE0000770	276	G1795	Plant growth and development	1-393	Arabidopsis thaliana
884	PHE0000771	277	G977	Plant growth and development	1-543	Arabidopsis thaliana
885	PHE0000772	278	G568	Plant growth and development	1-858	Arabidopsis thaliana
886	PHE0000773	279	G1269	Plant growth and development	1-861	Arabidopsis thaliana
887	PHE0000774	280	G1050	Plant growth and development	1-1557	Arabidopsis thaliana
888	PHE0000779	281	yeast GPA2	Stress tolerance	1-1347	Saccharomyces cerevisiae
889	PHE0000796	282	phytosulfokine 4 - 13399211	Plant growth and development	67-315	Oryza sativa

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
890	PHE0000797	283	rice phytosulfokine 2 - 13399209	Plant growth and development	107-463	Oryza sativa
891	PHE0000798	284	rice phytosulfokine-alpha - 11907498	Plant growth and development	102-368	Oryza sativa
892	PHE0000799	285	rice phytosulphokine SH27A - 3201971	Plant growth and development	9-314	Oryza sativa
893	PHE0000800	286	AtSUC1	Carbon and/or nitrogen metabolism	1-1539	Arabidopsis thaliana
894	PHE0000801	287	Arabidopsis SUT2	Carbon and/or nitrogen metabolism	1-1773	Arabidopsis thaliana
895	PHE0000802	288	Arabidopsis SUT4	Carbon and/or nitrogen metabolism	1-1530	Arabidopsis thaliana
896	PHE0000803	289	OsSUT1 - D87819	Carbon and/or nitrogen metabolism	67-1680	Oryza sativa
897	PHE0000804	290	OsSUT3 - AB071809	Carbon and/or nitrogen metabolism	85-1605	Oryza sativa
898	PHE0000805	291	Aspergillis phytochrome	Light response	1-2013	Emericella nidulans
899	PHE0000806	292	corn histidine phosphotransfer protein 1	Plant growth and development	103-561	Zea mays
900	PHE0000807	293	corn histidine phosphotransfer protein 2	Plant growth and development	57-512	Zea mays
901	PHE0000808	294	soy histidine phosphotransfer protein 1	Plant growth and development	63-527	Glycine max
902	PHE0000809	295	YPD1 - Z74283	Plant growth and development	320-823	Saccharomyces cerevisiae
903	PHE0000810	296	rice ethylene receptor - AF013979	Plant growth and development	66-1976	Oryza sativa
904	PHE0000811	297	rice ethylene responsive factor - AAK70909	Plant growth and development	9-917, 1160-1528, 1646-1912, 2188-2312, 2425-2662	Oryza sativa
905	PHE0000812	298	CYP79F1 (supershoot) - AF370512	Plant growth and development	75-1688	Arabidopsis thaliana
906	PHE0000813	299	AtSUC2	Carbon and/or nitrogen metabolism	1-1536	Arabidopsis thaliana
907	PHE0000814	300	soy G28 like	Stress tolerance	1-753	Glycine max
908	PHE0000815	301	corn G1792-like 2	Stress tolerance	104-661	Zea mays
909	PHE0000816	302	G1792	Stress tolerance	77-493	Arabidopsis thaliana

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
910	PHE0000817	303	corn duf6 2	Carbon and/or nitrogen metabolism	54-1394	Zea mays
911	PHE0000818	304	corn duf6 3	Carbon and/or nitrogen metabolism	30-1112	Zea mays
912	PHE0000819	305	corn duf6	Carbon and/or nitrogen metabolism	62-1324	Zea mays
913	PHE0000820	306	corn duf6 6	Carbon and/or nitrogen metabolism	174-1271	Zea mays
914	PHE0000822	307	corn duf6 11	Carbon and/or nitrogen metabolism	5-1072	Zea mays
915	PHE0000823	308	corn duf6 12	Carbon and/or nitrogen metabolism	113-1261	Zea mays
916	PHE0000824	309	corn duf6 13	Carbon and/or nitrogen metabolism	48-1127	Zea mays
917	PHE0000825	310	corn duf6 14	Carbon and/or nitrogen metabolism	112-1290	Zea mays
918	PHE0000826	311	corn duf6 15	Carbon and/or nitrogen metabolism	197-1327	Zea mays
919	PHE0000827	312	corn duf6 16	Carbon and/or nitrogen metabolism	111-1142	Zea mays
920	PHE0000828	313	corn duf6 17	Carbon and/or nitrogen metabolism	6-1097	Zea mays
921	PHE0000829	314	corn duf6 18	Carbon and/or nitrogen metabolism	149-1375	Zea mays
922	PHE0000830	315	corn duf6 19	Carbon and/or nitrogen metabolism	153-1193	Zea mays
923	PHE0000831	316	corn duf6 20	Carbon and/or nitrogen metabolism	145-1641	Zea mays
924	PHE0000832	317	soy duf6 1	Carbon and/or nitrogen metabolism	52-1170	Glycine max
925	PHE0000833	318	soy duf6 2	Carbon and/or nitrogen metabolism	151-1203	Glycine max

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
926	PHE0000834	319	soy duf6 3	Carbon and/or nitrogen metabolism	36-1073	Glycine max
927	PHE0000835	320	soy duf6 4	Carbon and/or nitrogen metabolism	69-1118	Glycine max
928	PHE0000836	321	soy duf6 5	Carbon and/or nitrogen metabolism	55-1140	Glycine max
929	PHE0000837	322	soy duf6 6	Carbon and/or nitrogen metabolism	36-1271	Glycine max
930	PHE0000838	323	soy duf6 7	Carbon and/or nitrogen metabolism	228-1226	Glycine max
931	PHE0000839	324	soy duf6 8	Carbon and/or nitrogen metabolism	140-1126	Glycine max
932	PHE0000840	325	soy duf6 9	Carbon and/or nitrogen metabolism	61-1173	Glycine max
933	PHE0000841	326	soy duf6 10	Carbon and/or nitrogen metabolism	99-1265	Glycine max
934	PHE0000842	327	soy duf6 11	Carbon and/or nitrogen metabolism	167-1084	Glycine max
935	PHE0000843	328	soy duf6 12	Carbon and/or nitrogen metabolism	158-1258	Glycine max
936	PHE0000844	329	soy duf6 13	Carbon and/or nitrogen metabolism	250-1284	Glycine max
937	PHE0000845	330	soy duf6 15	Carbon and/or nitrogen metabolism	96-1157	Glycine max
938	PHE0000846	331	rice Crinkly4 - AB057787	Seed development	805-3510	Oryza sativa
939	PHE0000847	332	rice S-domain receptor-like protein kinase 1-BAA94516	Seed development	89-2395	Oryza sativa
940	PHE0000848	333	rice S-domain receptor-like protein kinase 2 - BAB07906.1	Seed development	89-2437	Oryza sativa
941	PHE0000849	334	rice S-domain receptor-like protein kinase 3 - BAB07905.1	Seed development	98-2539	Oryza sativa
942	PHE0000850	335	rice S-domain receptor-like protein kinase 4 - BAB07904.1	Seed development	72-2321	Oryza sativa

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
943	PHE0000851	336	rice S-domain receptor-like protein kinase 5	Seed development	28-44, 145-173, 272-397, 1180-3476	Oryza sativa
944	PHE0000852	337	rice S-receptor kinase PK3 - BAB64641.1	Seed development	67-2562	Oryza sativa
945	PHE0000853	338	OsPK10 - L27821	Seed development	1-2475	Oryza sativa
946	PHE0000854	339	soy 14-3-3 22	Stress tolerance	32-802	Glycine max
947	PHE0000855	340	soy 14-3-3 22 N-terminus	Stress tolerance	32-382	Glycine max
948	PHE0000856	341	14-3-3-like protein N-terminus	Stress tolerance	6-365	Oryza sativa
949	PHE0000857	342	sorghum 14-3-3 10	Stress tolerance	116-874	Sorghum bicolor
950	PHE0000858	343	sorghum 14-3-3 10 N-terminus	Stress tolerance	116-460	Sorghum bicolor
951	PHE0000859	344	rice 14-3-3 15	Stress tolerance	70-855	Oryza sativa
952	PHE0000860	345	rice 14-3-3 15 N-terminus	Stress tolerance	70-429	Oryza sativa
953	PHE0000861	346	corn 14-3-3 13	Stress tolerance	62-808	Zea mays
954	PHE0000862	347	corn 14-3-3 13 N-terminus	Stress tolerance	62-409	Zea mays
955	PHE0000863	348	14-3-3 protein N-terminus	Stress tolerance	42-389	Glycine max
956	PHE0000864	349	rice 14-3-3 10	Stress tolerance	105-875	Oryza sativa
957	PHE0000865	350	rice 14-3-3 10 N-terminus	Stress tolerance	105-449	Oryza sativa
958	PHE0000866	351	soy 14-3-3 21	Stress tolerance	84-860	Glycine max
959	PHE0000867	352	soy 14-3-3 21 N-terminus	Stress tolerance	84-443	Glycine max
960	PHE0000868	353	wheat 14-3-3 10	Stress tolerance	64-840	Triticum aestivum
961	PHE0000869	354	wheat 14-3-3 10 N-terminus	Stress tolerance	64-420	Triticum aestivum
962	PHE0000870	355	corn 14-3-3 17	Stress tolerance	132-929	Zea mays
963	PHE0000871	356	corn 14-3-3 17 N-terminus	Stress tolerance	132-506	Zea mays
964	PHE0000872	357	rice G alpha XL - BAA93022	Plant growth and development	48-1040, 1127-1264, 2100-2204, 2500-2682, 3113-3290, 3374-3618, 3937-4109, 4430-4627, 4988-5378	Oryza sativa
965	PHE0000873	358	yeast casein kinase II alpha - CAA86916	Flower development	2-1120	Saccharomyces cerevisiae
966	PHE0000874	359	rice casein kinase alpha subunit - AAL34126	Flower development	29-363, 471-600, 1034-1228, 2564-2721, 3082-3172, 3250-3315, 3657-3739, 3821-3884, 3967-4035, 4124-4159	Oryza sativa

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
967	PHE0000875	360	soy casein kinase alpha	Flower development	129-1127	Glycine max
968	PHE0000876	361	rice casein kinase II beta subunit - AAG60201	Flower development	52-262, 2992-3213, 3477-3586, 3679-3844, 4365-4498	Oryza sativa
969	PHE0000877	362	yeast CKB1 - Z72541	Flower development	286-1122	Saccharomyces cerevisiae
970	PHE0000878	363	corn casein kinase beta 1	Flower development	231-1055	Zea mays
971	PHE0000879	364	corn casein kinase beta 2	Flower development	178-993	Zea mays
972	PHE0000884	365	CAR1-like 1	Stress tolerance	82-546	Zea mays
973	PHE0000885	366	corn CAR1-like 3	Stress tolerance	161-775	Zea mays
974	PHE0000886	367	corn CAR1-like 4	Stress tolerance	192-659	Zea mays
975	PHE0000887	368	corn CAR1-like 5	Stress tolerance	86-484	Zea mays
976	PHE0000888	369	yeast hnRNP methyltransferase-CAA53689	Stress tolerance	76-1122	Saccharomyces cerevisiae
977	PHE0000889	370	corn arginine N-methyl transferase 1	Stress tolerance	44-1318	Zea mays
978	PHE0000890	371	corn arginine N-methyl transferase 2	Stress tolerance	102-1232	Zea mays
979	PHE0000891	372	CAR1 - corn ABA inducible RNA-binding protein	Stress tolerance	68-538	Zea mays
980	PHE0000892	373	corn RING finger 100	Plant growth and development	292-1404	Zea mays
981	PHE0000893	374	corn RING finger 101	Plant growth and development	103-1077	Zea mays
982	PHE0000894	375	corn RING finger 103	Plant growth and development	20-1093	Zea mays
983	PHE0000895	376	corn RING finger 102	Plant growth and development	252-1295	Zea mays
984	PHE0000896	377	corn RING finger 104	Plant growth and development	293-925	Zea mays
985	PHE0000897	378	corn RING finger 105	Plant growth and development	95-934	Zea mays
986	PHE0000898	379	corn RING finger 106	Plant growth and development	99-563	Zea mays
987	PHE0000899	380	corn RING finger 108	Plant growth and development	308-1054	Zea mays
988	PHE0000900	381	corn RING finger 109	Plant growth and development	71-622	Zea mays
989	PHE0000901	382	corn RING finger 110 [ReMembR-H2 protein JR702]-	Plant growth and development	215-1756	Zea mays
990	PHE0000902	383	corn RING finger 111	Plant growth and development	162-599	Zea mays

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
991	PHE0000903	384	corn RING finger 112	Plant growth and development	411-2375	Zea mays
992	PHE0000904	385	corn RING finger 113	Plant growth and development	269-1828	Zea mays
993	PHE0000905	386	corn RING finger 114	Plant growth and development	167-781	Zea mays
994	PHE0000906	387	corn RING finger 115	Plant growth and development	294-806	Zea mays
995	PHE0000907	388	corn RING finger 116	Plant growth and development	187-1374	Zea mays
996	PHE0000908	389	corn Skp1-like 118 [UIP2]	Plant growth and development	94-597	Zea mays
997	PHE0000909	390	corn Skp1-like 119	Plant growth and development	158-1159	Zea mays
998	PHE0000910	391	corn Skp1-like 120 [UIP2]	Plant growth and development	106-633	Zea mays
999	PHE0000911	392	corn F-box 123	Plant growth and development	184-1980	Zea mays
1000	PHE0000912	393	corn F-box 124 [TIR1]	Plant growth and development	167-1936	Zea mays
1001	PHE0000913	394	corn F-box 125 [TIR1]	Plant growth and development	174-1892	Zea mays
1002	PHE0000914	395	corn F-box 126	Plant growth and development	107-1894	Zea mays
1003	PHE0000915	396	corn RING finger 128 [response regulator 6]	Plant growth and development	42-746	Zea mays
1004	PHE0000916	397	corn RING finger 132	Plant growth and development	107-985	Zea mays
1005	PHE0000917	398	corn RING finger 133	Plant growth and development	597-1496	Zea mays
1006	PHE0000918	399	corn ASH1	Stress tolerance	144-899	Zea mays
1007	PHE0000919	400	corn RING finger 136	Plant growth and development	95-1012	Zea mays
1008	PHE0000920	401	corn RING finger 138	Plant growth and development	117-902	Zea mays
1009	PHE0000921	402	corn F-box 141	Plant growth and development	487-1428	Zea mays
1010	PHE0000922	403	corn F-box 142	Plant growth and development	227-1114	Zea mays
1011	PHE0000923	404	corn F-box 143	Plant growth and development	352-1410	Zea mays
1012	PHE0000924	405	corn F-box 144	Plant growth and development	96-1406	Zea mays
1013	PHE0000925	406	corn F-box 145	Plant growth and development	436-1524	Zea mays
1014	PHE0000926	407	corn RING finger 147	Plant growth and development	79-927	Zea mays

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
1015	PHE0000927	408	corn RING finger 149 [anaphase promoting complex subunit 11]-	Plant growth and development	128-379	Zea mays
1016	PHE0000928	409	corn RING finger 151 [ROC1]	Plant growth and development	77-442	Zea mays
1017	PHE0000929	410	corn U-box 153	Plant growth and development	166-1743	Zea mays
1018	PHE0000930	411	corn RING finger 154 [VIP2]	Plant growth and development	262-1560	Zea mays
1019	PHE0000931	412	corn RING finger 155 [VIP2]	Plant growth and development	161-1498	Zea mays
1020	PHE0000932	413	rice U-box 100	Plant growth and development	121-939	Oryza sativa
1021	PHE0000933	414	corn RING finger protein 157	Plant growth and development	168-857	Zea mays
1022	PHE0000934	415	corn F-box 159 [FKF1-like]	Plant growth and development	195-2021	Zea mays
1023	PHE0000935	416	corn F-box 160 [FKF-like]	Plant growth and development	77-1930	Zea mays
1024	PHE0000936	417	corn RING finger 161 [cellulose synthase]	Plant growth and development	78-3026	Zea mays
1025	PHE0000937	418	corn RING finger 162 [cellulose synthase]	Plant growth and development	193-3414	Zea mays
1026	PHE0000938	419	corn RING finger 163	Plant growth and development	277-1059	Zea mays
1027	PHE0000939	420	corn RING finger 164	Plant growth and development	218-1033	Zea mays
1028	PHE0000940	421	corn RING finger 165	Plant growth and development	167-754	Zea mays
1029	PHE0000941	422	corn F-box 166	Plant growth and development	62-814	Zea mays
1030	PHE0000942	423	corn RING finger 167 [seven in absentia-like]	Plant growth and development	266-1288	Zea mays
1031	PHE0000943	424	corn F-box 168	Plant growth and development	203-1402	Zea mays
1032	PHE0000944	425	corn RING finger 169 [S-ribonuclease binding protein]	Plant growth and development	103-1113	Zea mays
1033	PHE0000945	426	corn F-box 170	Plant growth and development	123-1184	Zea mays
1034	PHE0000946	427	corn F-box 172	Plant growth and development	42-803	Zea mays
1035	PHE0000947	428	corn RING finger 174	Plant growth and development	255-1280	Zea mays
1036	PHE0000948	429	corn RING 175	Plant growth and development	179-1291	Zea mays
1037	PHE0000949	430	corn Cullin 176	Plant growth and development	221-931	Zea mays

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
1038	PHE0000950	431	corn RING finger 177	Plant growth and development	33-863	Zea mays
1039	PHE0000951	432	corn RING finger 178	Plant growth and development	227-1492	Zea mays
1040	PHE0000952	433	corn RING finger 179 [alpha-galactosidase]	Plant growth and development	68-1342	Zea mays
1041	PHE0000953	434	corn RING finger 180	Plant growth and development	265-1431	Zea mays
1042	PHE0000954	435	corn F-box 181	Plant growth and development	354-1397	Zea mays
1043	PHE0000955	436	corn RING finger 182	Plant growth and development	113-1282	Zea mays
1044	PHE0000956	437	corn RING finger 183	Plant growth and development	293-997	Zea mays
1045	PHE0000957	438	corn RING finger 185	Plant growth and development	104-829	Zea mays
1046	PHE0000958	439	corn F-box 186	Plant growth and development	47-1303	Zea mays
1047	PHE0000959	440	corn F-box 187	Plant growth and development	195-1199	Zea mays
1048	PHE0000960	441	corn RING/U-box 188	Plant growth and development	63-1142	Zea mays
1049	PHE0000961	442	corn SPS2-4	Carbon and/or nitrogen metabolism	105-3035	Zea mays
1050	PHE0000962	443	rice IRE1 - AB031396	Seed development	239-2920	Oryza sativa
1051	PHE0000963	444	rice IRE1 N-terminal domain - AB031396	Seed development	239-1483	Oryza sativa
1052	PHE0000964	445	rice IRE1 C-terminal domain - AB031396	Seed development	1481-2920	Oryza sativa
1053	PHE0000965	446	yeast IRE1 - P32361	Seed development	80-3427	Saccharomyces cerevisiae
1054	PHE0000966	447	yeast IRE1 N-terminal domain - P32361	Seed development	80-1798	Saccharomyces cerevisiae
1055	PHE0000967	448	yeast IRE1 C-terminal domain - P32361	Seed development	1799-3427	Saccharomyces cerevisiae
1056	PHE0000968	449	corn cytosine deaminase-like	Seed development	80-1339	Zea mays
1057	PHE0000969	450	corn aldose reductase	Seed development	106-1041	Zea mays
1058	PHE0000970	451	soy NADPH dependent mannose 6-phosphate reductase-	Seed development	32-958	Glycine max
1059	PHE0000972	453	yeast Ydr210w - NP_010496	Seed development	101-325	Saccharomyces cerevisiae
1060	PHE0000974	455	yeast Soh1 - NP_011388	Seed development	101-481	Saccharomyces cerevisiae

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
1061	PHE0000975	456	yeast TAD2 - NP_012499	Seed development	101-850	Saccharomyces cerevisiae
1062	PHE0000978	459	yeast Ynl010w - NP_014388	Seed development	101-823	Saccharomyces cerevisiae
1063	PHE0000979	460	yeast Ynl124w - NP_014275	Seed development	101-1576	Saccharomyces cerevisiae
1064	PHE0000980	461	yeast Ydl124w - NP_010159	Seed development	101-1036	Saccharomyces cerevisiae
1065	PHE0000984	465	yeast Glutaredoxin - NP_009895	Seed development	101-430	Saccharomyces cerevisiae
1066	PHE0000985	466	soy unknown protein	Seed development	228-1226	Saccharomyces cerevisiae
1067	PHE0000986	467	soy putative protein	Seed development	265-1002	Glycine max
1068	PHE0000987	468	corn CLC1	Stress tolerance	102-599	Zea mays
1069	PHE0000988	469	corn CLD1	Stress tolerance	69-461	Zea mays
1070	PHE0000989	470	rice Asr1 - AF039573	Stress tolerance	71-487	Oryza sativa
1071	PHE0000990	471	rice CLC1-like 1 - BAB19059	Stress tolerance	37-326, 451-703	Oryza sativa
1072	PHE0000991	472	corn Asr1-like 1	Stress tolerance	151-690	Zea mays
1073	PHE0000992	473	corn Asr1-like 5	Stress tolerance	89-511	Zea mays
1074	PHE0000993	474	corn sigma factor 1	Plant growth and development	219-1715	Zea mays
1075	PHE0000994	475	corn sigma factor 2 [Sig3]	Plant growth and development	166-1815	Zea mays
1076	PHE0000995	476	corn sigma factor 3 [Sig1]	Plant growth and development	101-1717	Zea mays
1077	PHE0000996	477	corn bromodomain protein	Seed development	417-2147	Zea mays
1078	PHE0000997	478	corn homeodomain leucine zipper protein	Seed development	292-1269	Zea mays
1079	PHE0000998	479	corn bZIP protein 3	Seed development	63-908	Zea mays
1080	PHE0000999	480	corn bZIP protein 4 [G-box binding factor 1]	Seed development	95-1225	Zea mays
1081	PHE0001000	481	corn remorin like DNA-binding protein 1	Seed development	84-1637	Zea mays
1082	PHE0001001	482	corn remorin like DNA-binding protein 2	Seed development	43-639	Zea mays
1083	PHE0001002	483	corn Gld-Tea protein 2	Seed development	47-811	Zea mays
1084	PHE0001003	484	corn homeobox protein 1	Seed development	370-1179	Zea mays
1085	PHE0001004	485	corn homeobox protein 3	Seed development	485-1300	Zea mays
1086	PHE0001005	486	corn heat shock transcription factor 1	Seed development	75-875	Zea mays

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
1087	PHE0001006	487	corn heat shock transcription factor 2	Seed development	895-1575	Zea mays
1088	PHE0001007	488	corn heat shock transcription factor 3	Seed development	195-965	Zea mays
1089	PHE0001008	489	corn heat shock transcription factor 4	Seed development	383-1276	Zea mays
1090	PHE0001009	490	corn IAA-like 1	Seed development	65-724	Zea mays
1091	PHE0001010	491	corn IAA-like 4	Seed development	762-1448	Zea mays
1092	PHE0001011	492	corn MADS box protein 100	Seed development	114-286, 383-819	Zea mays
1093	PHE0001012	493	corn MADS box protein 102	Seed development	293-1027	Zea mays
1094	PHE0001013	494	corn MADS box protein 103	Seed development	63-731	Zea mays
1095	PHE0001014	495	corn MADS box protein 104	Seed development	213-890	Zea mays
1096	PHE0001015	496	corn MADS box protein 105	Seed development	101-853	Zea mays
1097	PHE0001016	497	corn MADS box protein 108	Seed development	115-741	Zea mays
1098	PHE0001018	498	corn MADS box protein 114	Seed development	246-980	Zea mays
1099	PHE0001019	499	corn LIM domain protein 1	Seed development	99-1160	Zea mays
1100	PHE0001020	500	corn LIM domain protein 2	Seed development	171-782	Zea mays
1101	PHE0001021	501	corn myb-like DNA binding protein	Seed development	248-1105	Zea mays
1102	PHE0001022	502	corn myb domain protein 1	Seed development	112-945	Zea mays
1103	PHE0001023	503	corn myb domain protein 3	Seed development	125-1030	Zea mays
1104	PHE0001024	504	corn myb domain protein 4	Seed development	34-1101	Zea mays
1105	PHE0001025	505	corn NAM-like protein	Seed development	139-1563	Zea mays
1106	PHE0001026	506	corn transcriptional co-activator-like protein 1	Seed development	165-686	Zea mays
1107	PHE0001027	507	corn LSD1-like protein 1	Seed development	222-650	Zea mays
1108	PHE0001028	508	corn GS1-like protein	Seed development	84-806	Zea mays
1109	PHE0001029	509	corn RING finger 200	Seed development	268-1470	Zea mays
1110	PHE0001030	510	corn RING finger protein 202	Seed development	187-1158	Zea mays

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
1111	PHE0001031	511	corn PGPD14-like protein	Seed development	107-985	Zea mays
1112	PHE0001032	512	corn Ankyrin protein 1	Seed development	440-1891	Zea mays
1113	PHE0001033	513	corn zinc finger protein 10 [corn G325-like 3]	Seed development	424-1644	Zea mays
1114	PHE0001034	514	corn scarecrow protein 100	Seed development	242-1903	Zea mays
1115	PHE0001035	515	corn transcription elongation factor	Seed development	131-1234	Zea mays
1116	PHE0001036	516	corn constans-like protein 10	Seed development	128-904	Zea mays
1117	PHE0001037	517	corn copine-like protein 1	Seed development	518-1861	Zea mays
1118	PHE0001038	518	corn copine-like protein 2	Seed development	281-1513	Zea mays
1119	PHE0001039	519	corn RING finger protein 201	Seed development	311-1579	Zea mays
1120	PHE0001040	520	corn zinc finger protein	Seed development	65-1138	Zea mays
1121	PHE0001041	521	corn IAA-like 10	Seed development	146-823	Zea mays
1122	PHE0001042	522	corn constans-like 5	Seed development	215-829	Zea mays
1123	PHE0001043	523	soy G-gamma subunit DC-terminus	Plant growth and development	210-518	Glycine max
1124	PHE0001044	524	soy AGL8-like 1	Plant growth and development	346-1077	Glycine max
1125	PHE0001045	525	soy AGL8-like 3	Plant growth and development	147-863	Glycine max
1126	PHE0001046	526	corn Agl8D (LIB5131-001-H1)	Plant growth and development	1-735	Zea mays
1127	PHE0001047	527	corn Agl8E (LIB5131-001-H2)	Plant growth and development	1-798	Zea mays
1128	PHE0001048	528	corn Agl8F (LIB5131-001-H3)	Plant growth and development	1-798	Zea mays
1129	PHE0001050	529	Arabidopsis LFY	Flower development	40-1311	Arabidopsis thaliana
1130	PHE0001103	530	corn Isr	Plant growth and development	220-1254	Zea mays
1131	PHE0001104	531	soy Isr-like 1	Plant growth and development	365-1495	Glycine max
1132	PHE0001105	532	rice Isr-like 1	Plant growth and development	110-1159	Oryza sativa
1133	PHE0001160	533	soy G1792-like	Stress tolerance	20-391	Glycine max
1134	PHE0001161	534	corn sucrose export defective 1 (sdx1) - AF302187	Carbon and/or nitrogen metabolism	1-1425	Zea mays

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
1135	PHE0001162	535	rice sdx1 delta ctp	Carbon and/or nitrogen metabolism	345-409, 581-692, 710-827, 2019-2098, 3567-3646, 5059-5228, 5675-5772, 6541-6645, 7487-7603, 7908-8057, 9155-9328	Oryza sativa
1136	PHE0001163	536	Arabidopsis sucrose export defective 1-AF302188	Carbon and/or nitrogen metabolism	1-1467	Arabidopsis thaliana
1137	PHE0001164	537	Nostoc sp. PCC 7120 sdx1-like - 17134979	Carbon and/or nitrogen metabolism	1-1092	Nostoc PCC7120
1138	PHE0001165	538	Synechocystis sp. PCC 6803 sdx1-like - 1652844	Carbon and/or nitrogen metabolism	1-1092	Synechocystis sp. PCC 6803
1139	PHE0001166	539	Nostoc punctiforme sdx1-like	Carbon and/or nitrogen metabolism	294-1388	Nostoc punctiforme
1140	PHE0001173	540	corn CVY-CIK	Stress tolerance	217-1563	Zea mays
1141	PHE0001187	541	corn spa1-like	Light response	104-2467	Zea mays
1142	PHE0001188	542	corn calcium dependant protein kinase	Stress tolerance	649-2424	Zea mays
1143	PHE0001189	543	corn unknown protein	Stress tolerance	127-813	Zea mays
1144	PHE0001190	544	corn putative splicing factor	Stress tolerance	153-671	Zea mays
1145	PHE0001191	545	rice hydroxyproline-rich glycoprotein	Stress tolerance	120-1769	Oryza sativa
1146	PHE0001192	546	rice unknown protein - AAK14418	Stress tolerance	605-719, 800-864, 1161-1503, 1666-1732, 1833-1986, 2283-2450, 2553-2663, 2773-2883, 3025-3042, 3078-3179, 3748-3978, 4551-4625, 4905-4976, 5758-5943, 6029-6187, 6412-6504, 6891-6962, 7497-7587, 7830-8008, 8413-8494, 8687-8797, 8876-8982, 9355-9432, 9518-9613, 9788-9883, 11533-11700	Oryza sativa
1147	PHE0001193	547	corn unknown protein	Stress tolerance	87-1147, 1229-1919	Zea mays
1148	PHE0001194	548	corn alpha-amylase	Stress tolerance	553-1797	Zea mays
1149	PHE0001233	549	rice G1073-like 1	Plant growth and development	1-1008	Oryza sativa
1150	PHE0001234	550	rice inosine monophosphate dehydrogenase - AAK09225	Plant growth and development	45-1040, 2559-2738, 3841-4098, 4927-4998	Oryza sativa

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
1151	PHE0001235	551	yeast IMP dehydrogenase [Imd2p] - NP_012088	Plant growth and development	101-1669	Saccharomyces cerevisiae
1152	PHE0001236	552	E. coli guaB - NP_417003	Plant growth and development	1-1467	Escherichia coli
1153	PHE0001237	553	Agrobacterium GuaB - AE007996	Plant growth and development	7-1512	Agrobacterium tumefaciens
1154	PHE0001276	554	corn Transcription Factor #1	Seed development	1-921	Zea mays
1155	PHE0001277	555	corn Transcription Factor #2	Seed development	1-2028	Zea mays
1156	PHE0001325	556	corn RING finger protein 25	Plant growth and development	353-1771	Zea mays
1157	PHE0001326	557	yeast VHT1 - YGR065C	Carbon and/or nitrogen metabolism	101-1879	Saccharomyces cerevisiae
1158	PHE0001327	558	Arabidopsis Suc5 - AJ252133	Carbon and/or nitrogen metabolism	63-1592	Arabidopsis thaliana
1159	PHE0001400	559	soy G1792-like 2	Stress tolerance	18-431	Glycine max
1160	PHE0001401	560	corn G1792-like 3	Stress tolerance	247-639	Zea mays
1161	PHE0001423	561	Glutamate Decarboxylase	Plant growth and development	268-1761	Zea mays
1162	PHE0001432	562	putative carnitine/acylcarnitine translocase-	Plant growth and development	94-909	Zea mays
1163	PHE0001433	563	corn cycA-like [GATE80]	Plant growth and development	196-1230	Zea mays
1164	PHE0001434	564	corn cycA-like [GAT81]	Plant growth and development	188-1306	Zea mays
1165	PHE0001435	565	corn E4/E8 binding protein-like [GATE68]	Plant growth and development	253-2259	Zea mays
1166	PHE0001438	566	Arabidopsis G748	Plant growth and development	98-1441	Arabidopsis thaliana
1167	PHE0001439	567	Arabidopsis NAM (no apical meristem)-like protein-	Plant growth and development	175-1293	Arabidopsis thaliana
1168	PHE0001440	568	soy G1452-like protein	Plant growth and development	207-1319	Glycine max
1169	PHE0001497	569	corn cytochrome P450	Plant growth and development	143-1588	Zea mays
1170	PHE0001498	570	rice receptor-like protein	Plant growth and development	1-3885	Oryza sativa
1171	PHE0001499	571	rice receptor-like protein kinase	Plant growth and development	1-3333	Oryza sativa
1172	PHE0001500	572	rice putative brassinosteroid-insensitive protein	Plant growth and development	1-3366	Oryza sativa

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
1173	PHE0001501	573	rice cell elongation protein DIMINUTO	Plant growth and development	1-1686	Oryza sativa
1174	PHE0001502	574	corn Dwarf1-like 1	Plant growth and development	138-1823	Zea mays
1175	PHE0001503	575	rice putative sterol-C5(6)-desaturase	Plant growth and development	1-717	Oryza sativa
1176	PHE0001504	576	corn sterol-C5(6)-desaturase 2	Plant growth and development	60-881	Zea mays
1177	PHE0001505	577	corn sterol-C5(6)-desaturase 1	Plant growth and development	43-870	Zea mays
1178	PHE0001506	578	soy sterol-C5(6)-desaturase	Plant growth and development	158-1006	Glycine max
1179	PHE0001507	579	rice BRS1-like protease 4	Plant growth and development	78-1490	Oryza sativa
1180	PHE0001508	580	corn BRS1-like protease 1	Plant growth and development	109-1548	Zea mays
1181	PHE0001509	581	soy FKF1-like protein	Plant growth and development	19-1878	Glycine max
1182	PHE0001510	582	corn FKF-like protein 2	Plant growth and development	70-2115	Zea mays
1183	PHE0001542	583	yeast YDL168W/SFA1 - NP_010113	Nitric oxide signaling	101-1258	Saccharomyces cerevisiae
1184	PHE0001543	584	E. coli adhC - AE000142	Nitric oxide signaling	1-1110	Escherichia coli
1185	PHE0001544	585	Nostoc sp. PCC 7120 glutathione dependent formaldehyde dehydrogenase-BAB74509	Nitric oxide signaling	1-1110	Nostoc PCC7120
1186	PHE0001545	586	rice glutathione dependent formaldehyde dehydrogenase-U77637	Nitric oxide signaling	204-243, 391-527, 1160-1206, 1296-1621, 1946-2028, 2107-2182, 2805-2962, 3285-3446, 3541-3657	Oryza sativa
1187	PHE0001546	587	corn glutathione-dependent formaldehyde dehydrogenase-Y11029	Nitric oxide signaling	82-1227	Zea mays
1188	PHE0001547	588	corn corn glutathione-dependent formaldehyde dehydrogenase 2-	Nitric oxide signaling	108-1265	Zea mays
1189	PHE0001548	589	corn corn glutathione-dependent formaldehyde dehydrogenase 3-	Nitric oxide signaling	95-1231	Zea mays

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
1190	PHE0001549	590	soy glutathione dependent formaldehyde dehydrogenase-	Nitric oxide signaling	30-1166	Glycine max
1191	PHE0001550	591	rice putative phosphate translocator - AAK21346	Carbon and/or nitrogen metabolism	1-1113	Oryza sativa
1192	PHE0001551	592	rice glucose-6-phosphate/phosphate-tranlocator-13486660	Carbon and/or nitrogen metabolism	1-1071	Oryza sativa
1193	PHE0001552	593	corn glucose-6-phosphate/phosphate-tranlocator-	Carbon and/or nitrogen metabolism	165-1184	Zea mays
1194	PHE0001553	594	rice putative sugar transporter - AF416867	Carbon and/or nitrogen metabolism	3-1736	Oryza sativa
1195	PHE0001554	595	soy cycD4-like protein	Plant growth and development	222-1277	Glycine max
1196	PHE0001578	596	rice RPN12 - AB037153	Plant growth and development	76-879	Oryza sativa
1197	PHE0001579	597	YFR052W/RPN12 - NP_116710	Plant growth and development	101-922	Saccharomyces cerevisiae
1198	PHE0001580	598	corn rpn12	Plant growth and development	83-883	Zea mays
1199	PHE0001581	599	soy rpn12	Plant growth and development	113-913	Glycine max
1200	PHE0001583	600	sorghum TTG1-like	Stress tolerance	107-1288	Sorghum bicolor
1201	PHE0001584	601	corn TTG1-like protein 2	Stress tolerance	141-1388	Zea mays
1202	PHE0001595	602	ZmHK1	Plant growth and development	77-3001	Zea mays
1203	PHE0001596	603	Arabidopsis CRE1b	Plant growth and development	69-3311	Arabidopsis thaliana
1204	PHE0001597	604	Arabidopsis HK2	Plant growth and development	1-3531	Arabidopsis thaliana
1205	PHE0001598	605	Arabidopsis HK3	Plant growth and development	1-3111	Arabidopsis thaliana
1206	PHE0001607	606	maize nitrate transporter like 1 sequence	Seed development	494-2068	Zea mays
1207	PHE0001608	607	rice nitrate transporter like 1 sequence	Seed development	97-1698	Oryza sativa
1208	PHE0001609	608	rice nitrate transporter like 2 sequence	Seed development	1-1551	Oryza sativa
1209	PHE0001667	609	rice histidine kinase	Plant growth and development	201-3239	Oryza sativa
1210	PHE0002018	610	Arabidopsis nitrate transporter NTL1 like sequence	Seed development	76-1833	Arabidopsis thaliana

PEP SEQ ID NO:	Phe ID	NUC SEQ NO:	Gene Name	Gene Effect	Coding Sequence	Species
1211	PHE0002019	611	maize nitrate transporter NTL1 like sequence	Seed development	75-1907	Zea mays
1212	PHE0002020	612	maize nitrate transporter NTL1 like 2 sequence	Seed development	212-1954	Zea mays
1213	PHE0002021	613	rice nitrate transporter NTL1 like 1 sequence	Seed development	163-1944	Oryza sativa
1214	PHE0002022	614	rice nitrate transporter NTL1 like 2 sequence	Seed development	1-1743	Oryza sativa
1215	PHE0000372	22	G1073	Plant growth and development	1-810	Arabidopsis thaliana
1216	PHE0000493	67	Synechocystis ssr3189 - BAA17701	Stress tolerance	54-221	Synechocystis sp. PCC 6803
1217	PHE0000494	68	Synechocystis ssr2315 - BAA17190	Stress tolerance	242-457	Synechocystis sp. PCC 6803
1218	PHE0000522	95	wheat clv3-like	Plant growth and development	102-365	Triticum aestivum
1219	PHE0000524	97	corn ESR2	Plant growth and development	46-441	Zea mays
1220	PHE0000602	169	yeast BIR1	Plant growth and development	345-3209	Saccharomyces cerevisiae
1221	PHE0000765	271	G1073	Plant growth and development	1-810	Arabidopsis thaliana
1222	PHE0000971	452	yeast YBL107c - Z35868	Seed development	29-619	Saccharomyces cerevisiae
1223	PHE0000973	454	yeast YDR209c - S61572	Seed development	101-511	Saccharomyces cerevisiae
1224	PHE0000976	457	yeast Yet1 - NP_012858	Seed development	101-718	Saccharomyces cerevisiae
1225	PHE0000977	458	yeast Ylr162w - NP_013263	Seed development	101-454	Saccharomyces cerevisiae
1226	PHE0000981	462	yeast Ygr039w - NP_011553	Seed development	101-409	Saccharomyces cerevisiae
1227	PHE0000982	463	yeast Usa1 - NP_013683	Seed development	101-2614	Saccharomyces cerevisiae
1228	PHE0000983	464	yeast Ynr061c - NP_014459	Seed development	101-757	Saccharomyces cerevisiae

Transgenic plants having enhanced phenotypes are identified from populations of plants transformed as described herein by evaluating the phenotype in a variety of assays to detect an enhanced phenotype. These assays also may take many forms, including but not limited to, analyses to detect changes in the chemical composition, morphology, biomass or physiological responses of the plant to stress conditions. Enhanced physiological properties in transgenic plants of the present invention may be identified by evaluation of responses to stress conditions, for example in assays using imposed stress conditions to detect improved responses to water stress, nitrogen deficiency, cold growing conditions, pathogen or insect attack or light deficiency, or alternatively, under naturally present stress conditions, for example under field conditions. Enhanced chemical compositions, such as nutritional composition of grain, may be detected by analysis, for example, of composition and content of seed protein, free amino acids, oil, free fatty acids, starch or tocopherols. Biomass measures may be made on greenhouse or field grown plants and may include such measurements as plant height, stem diameter, root and shoot dry weights, and, for corn plants, ear length and diameter

Phenotypic data on morphological changes may be collected by visual observation during the process of plant regeneration as well as in regenerated plants transferred to soil. Such phenotypic data includes characteristics such as normal plants, bushy plants, taller plants, thicker stalks, narrow leaves, striped leaves, knotted phenotype, chlorosis, albino, anthocyanin production, or altered tassels, ears or roots. Other enhanced phenotypes may be identified by measurements taken under field conditions, such as days to pollen shed, days to silking, leaf extension rate, chlorophyll content, leaf temperature, stand, seedling vigor, internode length, plant height, leaf number, leaf area, tillering, brace roots, stay green, stalk lodging, root lodging, plant health, barreness/prolificacy, green snap, and pest resistance. In addition, phenotypic characteristics of harvested grain may be evaluated, including number of kernels per row on the ear, number of rows of kernels on the ear, kernel abortion, kernel weight, kernel size, kernel density and physical grain quality.

To confirm hybrid yield in transgenic corn plants expressing genes of the present invention, it may be desirable to test hybrids over multiple years at multiple locations in a geographical location where maize is conventionally grown, e.g. in Iowa, Illinois or other locations in the midwestern United States, under "normal" field conditions as well as under stress conditions, e.g. under drought or population density stress.

Of particular interest in the present invention are corn and soybean plants. Other plants of interest in the present invention for production of transgenic seed that can be grown to provide plants having enhanced properties include, without limitation, cotton, canola, wheat, sunflower, sorghum, alfalfa, barley, millet, rice, tobacco, fruit and vegetable crops, and turfgrass

Protein and Polypeptide Molecules

Polypeptides considered in the present invention are entire proteins or at least a sufficient portion of the entire protein to impart the relevant biological activity of the protein, e.g. enhanced plant phenotype. The term “protein” also includes molecules consisting of one or more polypeptide chains. Thus, a polypeptide useful in the present invention may constitute an entire protein having the desired biological activity, or may constitute a portion of an oligomeric protein having multiple polypeptide chains. Polypeptides useful for generation of transgenic plants having enhanced properties include the polypeptides provided herein as SEQ ID NO:614 through SEQ ID NO:1228, as well as homologs of such polypeptides.

Homologs of the polypeptides of the present invention may be identified by comparison of the amino acid sequence of the polypeptide to amino acid sequences of polypeptides from the same or different plant sources, e.g. manually or by using known homology-based search algorithms such as those commonly known and referred to as BLAST, FASTA, and Smith-Waterman. As used herein, a homolog is a peptide from the same or a different organism that performs the same biological function as the polypeptide to which it is compared. An orthologous relation between two organisms is not necessarily manifest as a one-to-one correspondence between two genes, because a gene can be duplicated or deleted after organism phylogenetic separation, such as speciation. For a given polypeptide, there may be no ortholog or more than one ortholog. Other complicating factors include alternatively spliced transcripts from the same gene, limited gene identification, redundant copies of the same gene with different sequence lengths or corrected sequence. A local sequence alignment program, e.g. BLAST, can be used to search a database of sequences to find similar sequences, and the summary Expectation value (E-value) used to measure the sequence base similarity. As a polypeptide hit with the best E-value for a particular organism may not necessarily be an ortholog or the only ortholog, a reciprocal BLAST search is used in the present invention to filter hit sequences with significant E-values for ortholog identification. The reciprocal BLAST entails search of the significant hits against a database of polypeptide sequences from the base organism that are similar to the sequence of the query polypeptide. A hit is a likely ortholog, when the reciprocal BLAST's best hit is the query polypeptide itself or a polypeptide encoded by a duplicated gene after speciation. Thus, homolog is used herein to described polypeptides that are assumed to have functional similarity by inference from sequence base similarity. Homologs of the polypeptides of the present invention are described in Table 2 provided on the CD-ROM provided herewith, and disclosed as SEQ ID NO:1229 through SEQ ID NO:27373.

A further aspect of the invention comprises functional homolog proteins which differ in one or more amino acids from those of a polypeptide provided herein as the result of one or more of the well-known conservative amino acid substitutions, e.g. valine is a conservative substitute for alanine and threonine is a conservative substitute for serine. Conservative substitutions for an amino acid within the native polypeptide sequence can be selected from other members of a class to which the naturally occurring amino acid belongs. Representative amino acids within these various classes include, but are not limited to: (1) acidic (negatively charged) amino acids such as aspartic acid and glutamic acid; (2) basic (positively charged) amino acids such as arginine, histidine, and lysine; (3) neutral polar amino acids such as glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; and (4) neutral nonpolar (hydrophobic) amino acids such as alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine. Conserved substitutes for an amino acid within a native amino acid sequence can be selected from other members of the group to which the naturally occurring amino acid belongs. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. Naturally conservative amino acids substitution groups are: valine-leucine, valine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, aspartic acid-glutamic acid, and asparagine-glutamine. A further aspect of the invention comprises polypeptides that differ in one or more amino acids from those of a described protein sequence as the result of deletion or insertion of one or more amino acids in a native sequence.

Homologs of the polypeptides provided herein will generally demonstrate significant identity with the polypeptides provided herein. Of particular interest are polypeptides having at least 50% sequence identity, more preferably at least about 70% sequence identity or higher, e.g. at least about 80% sequence identity with an amino acid sequence of SEQ ID NO:1 through SEQ ID NO:614. Of course useful polypeptides also include those with higher identity to such a polypeptide sequence, e.g. 90% to 99% identity. Identity of protein homologs is determined by optimally aligning the amino acid sequence of a putative protein homolog with a defined amino acid sequence and by calculating the percentage of identical and conservatively substituted amino acids over the window of comparison. Preferentially, the window of comparison for determining identity is the entire polypeptide sequence disclosed herein, e.g. the full sequence of any of SEQ ID NO:615 through SEQ ID NO:1228.

Recombinant Polynucleotides

The present invention contemplates the use of polynucleotides effective for imparting an enhanced phenotype to transgenic plants expressing said polynucleotides. Exemplary polynucleotides for use in the present invention are listed in Table 4 above and provided herein as SEQ ID NO:1 through SEQ ID NO:614. A subset of the nucleic molecules of this invention includes fragments of the disclosed polynucleotides consisting of oligonucleotides of at least 15, preferably at least 16 or 17, more preferably at least 18 or 19, and even more preferably at least 20 or more, consecutive nucleotides. Such oligonucleotides are fragments of the larger molecules having a sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO:614, and find use, for example as probes and primers for detection of the polynucleotides of the present invention.

Also of interest in the present invention are variants of the polynucleotides provided herein. Such variants may be naturally occurring, including homologous polynucleotides from the same or a different species, or may be non-natural variants, for example polynucleotides synthesized using chemical synthesis methods, or generated using recombinant DNA techniques. Degeneracy of the genetic code provides the possibility to substitute at least one base of the protein encoding sequence of a gene with a different base without causing the amino acid sequence of the polypeptide produced from the gene to be changed. Hence, a polynucleotide useful in the present invention may have any base sequence that has been changed from SEQ ID NO:1 to SEQ ID NO:614 by substitution in accordance with degeneracy of the genetic code.

Homologs of the polynucleotides provided herein will generally demonstrate significant identity with the polynucleotides provided herein. A polynucleotide of the present invention is substantially identical to a reference polynucleotide if, when the sequences of the polynucleotides are optimally aligned there is about 60% nucleotide equivalence; more preferably 70%; more preferably 80% equivalence; more preferably 85% equivalence; more preferably 90%; more preferably 95%; and/or more preferably 98% or 99% equivalence over a comparison window. A comparison window is preferably at least 50-100 nucleotides, and more preferably is the entire length of the polynucleotide provided herein. Optimal alignment of sequences for aligning a comparison window may be conducted by algorithms; preferably by computerized implementations of these algorithms (for example, the Wisconsin Genetics Software Package Release 7.0-10.0, Genetics Computer Group, 575 Science Dr., Madison, WI). The reference polynucleotide may be a full-length molecule or a portion of a longer molecule. Preferentially, the window of comparison for determining polynucleotide identity of protein encoding sequences is the entire coding region.

In a preferred embodiment, a polynucleotide of the present invention is operatively linked in a recombinant polynucleotide to a promoter functional in a plant to provide for expression of the polynucleotide in the sense orientation such that a desired polypeptide is produced. Also considered are embodiments wherein a polynucleotide is operatively linked to a promoter functional in a plant to provide for expression of the polynucleotide in the antisense orientation such that a complementary copy of at least a portion of an mRNA native to the target plant host is produced. Such a transcript may contain both sense and antisense regions of a polynucleotide, for example where RNAi methods are used for gene suppression.

Recombinant polynucleotides of the present invention are assembled in recombinant DNA constructs using methods known to those of ordinary skill in the art. Thus, transgenic DNA constructs used for transforming plant cells will comprise a polynucleotide one desires to introduce into a target plant. Such constructs will also typically comprise a promoter operatively linked to said polynucleotide to provide for expression in the target plant. Other construct components may include additional regulatory elements, such as 5' or 3' untranslated regions (such as polyadenylation sites), intron regions, and transit or signal peptides.

Numerous promoters that are active in plant cells have been described in the literature. These include promoters present in plant genomes as well as promoters from other sources, including nopaline synthase (NOS) promoter and octopine synthase (OCS) promoters carried on tumor-inducing plasmids of *Agrobacterium tumefaciens*, caulimovirus promoters such as the cauliflower mosaic virus or figwort mosaic virus promoters. For instance, see U.S. Patents No. 5,858,742 and 5,322,938 which disclose versions of the constitutive promoter derived from cauliflower mosaic virus (CaMV35S), US Patent No. 5,378,619 which discloses a Figwort Mosaic Virus (FMV) 35S promoter, U.S. Patent 6,437,217 which discloses a maize RS81 promoter, U.S. Patent 5,641,876 which discloses a rice actin promoter, U.S. Patent 6,426,446 which discloses a maize RS324 promoter, U.S. Patent 6,429,362 which discloses a maize PR-1 promoter, U.S. Patent 6,232,526 which discloses a maize A3 promoter, U.S. Patent 6,177,611 which discloses constitutive maize promoters, U.S. Patent 6,433,252 which discloses a maize L3 oleosin promoter, U.S. Patent 6,429,357 which discloses a rice actin 2 promoter and intron, U.S. Patent 5,837,848 which discloses a root specific promoter, U.S. Patent 6,084,089 which discloses cold inducible promoters, U.S. Patent 6,294,714 which discloses light inducible promoters, U.S. Patent 6,140,078 which discloses salt inducible promoters, U.S. Patent 6,252,138 which discloses pathogen inducible promoters, U.S. Patent 6,175,060 which discloses phosphorus deficiency inducible promoters, U.S. Patent Application Publication 2002/0192813A1 which discloses 5', 3' and intron elements useful in the design of effective plant expression vectors, U.S. patent application Serial No. 09/078,972 which discloses a coixin promoter, U.S. patent application Serial No. 09/757,089 which discloses a maize chloroplast aldolase promoter, all of which are incorporated herein by reference. These and numerous other promoters that function in plant cells are known to those skilled in the art and available for use in recombinant polynucleotides of the present invention to provide for expression of desired genes in transgenic plant cells.

Furthermore, the promoters may be altered to contain multiple "enhancer sequences" to assist in elevating gene expression. Such enhancers are known in the art. By including an enhancer sequence with such constructs, the expression of the selected protein may be enhanced. These enhancers often are found 5' to the start of transcription in a promoter that functions in eukaryotic cells, but can often be inserted in the forward or reverse orientation 5' or 3' to the coding sequence. In some instances, these 5' enhancing elements are introns. Deemed to be particularly useful as enhancers are the 5' introns of the rice actin 1 and rice actin 2 genes. Examples of other enhancers that can be used in accordance with the invention include elements from the CaMV 35S promoter, octopine synthase genes, the maize alcohol dehydrogenase gene, the maize shrunken 1 gene and promoters from non-plant eukaryotes.

In some aspects of the invention it is preferred that the promoter element in the DNA construct be capable of causing sufficient expression to result in the production of an effective amount of a polypeptide in water deficit conditions. Such promoters can be identified and isolated from the regulatory region of plant genes that are over expressed in water deficit conditions. Specific water-deficit-inducible promoters for use in this invention are derived from the 5' regulatory region of genes identified as a heat shock protein 17.5 gene *(HSP17.5)*, an HVA22 gene *(HVA22)*, and a cinnamic acid 4-hydroxylase (CA4H) gene *(CA4H)* of *Zea maize*. Such water-deficit-inducible promoters are disclosed in U.S. provisional application Serial No. 60/435,987, filed December 20, 2002, incorporated herein by reference.

In other aspects of the invention, sufficient expression in plant seed tissues is desired to effect improvements in seed composition. Exemplary promoters for use for seed composition modification include promoters from seed genes such as napin (U.S. Patent 5,420,034), oleosin, zein Z27 (Russell *et al.* (1997) *Transgenic Res.* 6(2):157-166), globulin 1 (Belanger *et al* (1991) Genetics 129:863-872), glutelin 1 (Russell (1997) *supra*), and peroxiredoxin antioxidant (Per1) (Stacy *et al.* (1996) *Plant Mol Biol.* 31(6):1205-1216).

In still other aspects of the invention, preferential expression in plant green tissues is desired. Promoters of interest for such uses include those from genes such as SSU (Fischhoff *et al.* (1992) Plant Mol Biol. 20:81-93), aldolase and pyruvate orthophosphate dikinase (PPDK) (Taniguchi *et al.* (2000) *Plant Cell Physiol.* 41(1):42-48).

Recombinant constructs prepared in accordance with the invention will also generally include a 3' untranlated DNA region that typically contains a polyadenylation sequence following the polynucleotide coding region. Examples of useful 3' UTRs include those from the nopaline synthase gene of *Agrobacterium tumefaciens* (*nos*), a gene encoding the small subunit of a ribulose-1,5-bisphosphate carboxylase-oxygenase (rbcS), and the T7 transcript of *Agrobacterium tumefaciens*.

Constructs and vectors may also include a transit peptide for targeting of a gene target to a plant organelle, particularly to a chloroplast, leucoplast or other plastid organelle. For descriptions of the use of chloroplast transit peptides see U.S. Patent 5, 188,642 and U.S. Patent No. 5,728,925, incorporated herein by reference. For description of the transit peptide region of an Arabidopsis EPSPS gene useful in the present invention, see Klee, H.J. *et al* (MGG (1987) 210:437-442).

The present invention also encompasses transgenic plants with stacked engineered traits, e.g. a crop having an enhanced phenotype resulting from expression of a recombinant polynucleotide provided herein, in combination with herbicide and/or pest resistance traits. For example, genes of the current invention can be stacked with other traits of agronomic interest, such as a trait providing herbicide resistance, for example a RoundUp Ready trait, or insect resistance, such as using a gene from *Bacillus thuringensis* to provide resistance against lepidopteran, coliopteran, homopteran, hemiopteran, and other insects. Herbicides for which resistance is useful in a plant include glyphosate herbicides, phosphinothricin herbicides, oxynil herbicides, imidazolinone herbicides, dinitroaniline herbicides, pyridine herbicides, sulfonylurea herbicides, bialaphos herbicides, sulfonamide herbicides and gluphosinate herbicides. To illustrate the that production of transgenic plants with herbicide resistance is a capability of those of ordinary skill in the art reference is made to U.S. patent application publications 2003/0106096A1 and 2002/0112260A1 and U.S. Patents 5,034,322; 5,776,760, 6,107,549 and 6,376,754, all of which are incorporated herein by reference. To illustrate that the production of transgenic plants with pest resistance is a capability of those of ordinary skill in the art reference is made to U.S. Patents 5,250,515 and 5,880,275 which disclose plants expressing an endotoxin of *Bacillus thuringiensis* bacteria, to U.S. Patent 6,506,599 which discloses control of invertebrates which feed on transgenic plants which express dsRNA for suppressing a target gene in the invertebrate, to U.S. Patent 5,986,175 which discloses the control of viral pests by transgenic plants which express viral replicase, and to U.S. Patent Application Publication 2003/0150017 A1 which discloses control of pests by a transgenic plant which express a dsRNA targeted to suppressing a gene in the pest, all of which are incorporated herein by reference.

Plant Transformation Constructs and Methods

Constructs used for transforming plant cells will comprise the recombinant polynucleotide that one desires to introduce as well as various other elements as described above. It is also contemplated that one may employ multiple genes for expression of multiple polynucleotides for crop improvement provided herein or for expression of a polynucleotide provided herein and one or more other desirable genes on either the same or different vectors for transformation. In the latter case, the different vectors may be delivered concurrently to recipient cells if co-transformation into a single chromosomal location is desired. Numerous methods for transforming plant cells with recombinant DNA are known in the art and may be used in the present invention. Two commonly used methods for plant transformation are *Agrobacterium-*

mediated transformation and microprojectile bombardment. Microprojectile bombardment methods are illustrated in U.S. Patents 5,015,580; 5,550,318; 5,538,880; 5,914,451; 6,160,208; 6,399,861 and 6,403,865 and *Agrobacterium*-mediated transformation is described in U.S. Patents 5,635,055; 5,824,877; 5,591,616; 5,981,840 and 6,384,301, all of which are incorporated herein by reference. For *Agrobacterium tumefaciens* based plant transformation system, additional elements present on transformation constructs will include T-DNA left and right border sequences to facilitate incorporation of the recombinant polynucleotide into the plant genome.

In general it is preferred to introduce heterologous DNA randomly, i.e. at a non-specific location, in the genome of a target plant line. In special cases it may be useful to target heterologous DNA insertion in order to achieve site-specific integration, e.g. to replace an existing gene in the genome, to use an existing promoter in the plant genome, or to insert a recombinant polynucleotide at a predetermined site known to be active for gene expression. Several site specific recombination systems exist which are known to function implants include cre-lox as disclosed in U.S. Patent 4,959,317 and FLP-FRT as disclosed in U.S. Patent 5,527,695, both incorporated herein by reference.

Transformation methods of this invention are preferably practiced in tissue culture on media and in a controlled environment. "Media" refers to the numerous nutrient mixtures that are used to grow cells *in vitro*, that is, outside of the intact living organism. Recipient cell targets include, but are not limited to, meristem cells, callus, immature embryos and gametic cells such as microspores, pollen, sperm and egg cells. It is contemplated that any cell from which a fertile plant may be regenerated is useful as a recipient cell. Callus may be initiated from tissue sources including, but not limited to, immature embryos, seedling apical meristems, microspores and the like. Cells capable of proliferating as callus are also recipient cells for genetic transformation. Practical transformation methods and materials for making transgenic plants of this invention, e.g. various media and recipient target cells, transformation of immature embryos and subsequent regeneration of fertile transgenic plants are disclosed in U.S. Patents 6,194,636 and 6,232,526 and U.S. patent application Serial No. 09/757,089, which are incorporated herein by reference.

In practice DNA is introduced into only a small percentage of target cells in any one experiment. Marker genes are used to provide an efficient system for identification of those cells that are stably transformed by receiving and integrating a transgenic DNA construct into their genomes. Preferred marker genes provide selective markers that confer resistance to a selective agent, such as an antibiotic or herbicide. Potentially transformed cells are exposed to the selective agent. In the population of surviving cells will be those cells where, generally, the resistance-conferring gene has been integrated and expressed at sufficient levels to permit cell survival. Cells may be tested further to confirm stable integration of the exogenous DNA. Useful selective marker genes include those conferring resistance to antibiotics such as kanamycin (*nptII*), hygromycin B (*aph IV*) and gentamycin (*aac3* and *aac*C4) or resistance to herbicides such as glufosinate (*bar* or *pat*) and glyphosate (EPSPS). Examples of such selectable are illustrated in U.S. Patents 5,550,318; 5,633,435; 5,780,708 and 6,118,047, all of which are incorporated herein by reference. Screenable markers which provide an ability to visually identify transformants can also be employed, *e.g.*, a gene expressing a colored or fluorescent protein such as a luciferase or green fluorescent protein (GFP) or a gene expressing a *beta*-glucuronidase or *uid*A gene (GUS) for which various chromogenic substrates are known. It is also contemplated that combinations of screenable and selectable markers will be useful for identification of transformed cells. See PCT publication WO 99/61129 which discloses use of a gene fusion between a selectable marker gene and a screenable marker gene, e.g. an NPTII gene and a GFP gene.

Cells that survive exposure to the selective agent, or cells that have been scored positive in a screening assay, may be cultured in regeneration media and allowed to mature into plants. Developing plantlets can be transferred to soil less plant growth mix, and hardened off, *e.g.*, in an environmentally controlled chamber at about 85% relative humidity, 600 ppm CO_2, and 25-250 microeinsteins $m^{-2} s^{-1}$ of light, prior to transfer to a greenhouse or growth chamber for maturation. Plants are preferably matured either in a growth chamber or greenhouse. Plants are regenerated from about 6 wk to 10 months after a transformant is identified, depending on the initial tissue. During regeneration, cells are grown to plants on solid media at about 19 to 28°C. After regenerating plants have reached the stage of shoot and root development, they may be transferred to a greenhouse for further growth and testing. Plants may be pollinated using conventional plant breeding methods known to those of skill in the art and seed produced.

Progeny may be recovered from transformed plants and tested for expression of the exogenous recombinant polynucleotide. Useful assays include, for example, "molecular biological" assays, such as Southern and Northern blotting and PCR; "biochemical" assays, such as detecting the presence of RNA, e.g. double stranded RNA, or a protein product, *e.g.*, by immunological means (ELISAs and Western blots) or by enzymatic function; plant part assays, such as leaf or root assays; and also, by analyzing the phenotype of the whole regenerated plant.

The present invention will be further illustrated by means of the following examples provided for illustration purposes only and in no way intended to limit the scope of the invention.

EXAMPLES

Example 1 Constructs for Maize Transformation

A GATEWAY™ Destination (Invitrogen Life Technologies, Carlsbad, CA) plant expression vector, pMON65154, was constructed for use in preparation of constructs comprising recombinant polynucleotides for corn transformation. The elements of the expression vector are summarized in Table 5 below. Generally, pMON65154 comprises a selectable marker expression cassette comprising a Cauliflower Mosaic Virus 35S promoter operably linked to a gene encoding neomycin phosphotransferase II (*npt*II). The 3' region of the selectable marker expression cassette comprises the 3' region of the *Agrobacterium tumefaciense* nopaline synthase gene (*nos*) followed 3' by the 3' region of the potato proteinase inhibitor II (*pin*II) gene. The plasmid pMON 65154 further comprises a plant expression cassette into which a gene of interest may be inserted using GATEWAY™ cloning methods. The GATEWAY™ cloning cassette is flanked 5' by a rice actin 1 promoter, exon and intron and flanked 3' by the 3' region of the potato *pin*II gene. Using GATEWAY™ methods, the cloning cassette may be replaced with a gene of interest. The vector pMON65154, and derivatives thereof comprising a gene of interest, are particularly useful in methods of plant transformation via direct DNA delivery, such as microprojectile bombardment.

Table 5 Elements of Plasmid pMON65154

FUNCTION	ELEMENT	REFERENCE
Plant gene of interest expression cassette	Rice actin 1 promoter	U.S. Patent 5,641,876
	Rice actin 1 exon 1, intron 1 enhancer	U.S. Patent 5,641,876
Gene of interest insertion site	*Att*R1	GATEWAY™Cloning Technology Instruction Manual
	CmR gene	GATEWAY™Cloning Technology Instruction Manual
	*ccd*A, *ccd*B genes	GATEWAY™Cloning Technology Instruction Manual
	*att*R2	GATEWAY™Cloning Technology Instruction Manual
Plant gene of interest expression cassette	Potato pinII 3' region	An *et al.* (1989) Plant Cell 1:115-122
Plant selectable marker expression cassette	CaMV 35S promoter	U.S. Patent 5,858,742
	nptII selectable marker	U.S. Patent 5,858,742
	nos 3' region	U.S. Patent 5,858,742
	PinII 3' region	An *et al.* (1989) Plant Cell 1:115-122
Maintenance in *E. coli*	*ColE1* origin of replication	
	F1 origin of replication	
	Bla ampicillin resistance	

A similar plasmid vector, pMON72472, is constructed for use in *Agrobacterium* mediated methods of plant transformation. pMON72472 comprises the gene of interest plant expression cassette, GATEWAY™ cloning, and plant selectable marker expression cassettes present in pMON65154. In addition, left and right T-DNA border sequences from *Agrobacterium* are added to the plasmid (Zambryski *et al.* (1982)). The right border sequence is located 5' to the rice actin 1 promoter and the left border sequence is located 3' to the *pin*II 3' sequence situated 3' to the *npt*II gene. Furthermore, pMON72472 comprises a plasmid backbone to facilitate replication of the plasmid in both *E. coli* and *Agrobacterium tumefaciens*. The backbone has an *ori*V wide host range origin of DNA replication functional in *Agrobacterium*, a pBR322 origin of replication functional in *E.coli*, and a spectinomycin/stretptomycin resistance gene for selection in both *E. coli* and *Agrobacterium*.

Vectors similar to those described above may be constructed for use in *Agrobacterium* or microprojectile bombardment maize transformation systems where the rice actin 1 promoter in the plant expression cassette portion is replaced with other desirable promoters including, but not limited to a maize globulin 1 promoter, a maize oleosin promoter, a glutelin 1 promoter, an aldolase promoter, a zein Z27 promoter, a pyruvate orthophosphate dikinase (PPDK) promoter, a a soybean 7S alpha promoter, a peroxiredoxin antioxidant (Per1) promoter and a CaMV 35S promoter. Protein coding segments are amplified by PCR prior to insertion into vectors such as described above. Primers for PCR amplification can be designed at or near the start and stop codons of the coding sequence, in order to eliminate most of the 5' and 3' untranslated regions. For GATEWAY cloning methods, PCR products are tailed with *att*B1 and *att*B2 sequences, purified then recombined into a destination vectors to produce an expression vector for use in transformation.

Exemplary constructs for transformation of maize to produce plants having enhanced phenotypes are provided in Table 6 below.

"SEQ ID NO" refers to a particular nucleic acid sequence in the Sequence Listing which defines a polynucleotide used in a recombinant polynucleotide of this invention.
"PHE ID" refers to an arbitrary number used to identify a particular recombinant polynucleotide corresponding to the translated protein encoded by the polynucleotide.
"NOM ID" refers to a particular construct comprising a polynucleotide of this invention.
"GENE NAME" refers to a common name for the recombinant polynucleotide.
"PROMOTER" provides the name of the promoter region driving expression of the polynucleotide
"TARGET" indicates if a chloroplast transit peptide is employed in the construct
"pMON" refers to an arbitrary number used to designate a particular recombinant DNA construct. Constructs are prophetic where no pMON is provided.

TABLE 6 Maize Transformation Constructs

SEQ ID NO	Phe ID	Nom ID	Gene Name	Promoter	Target	pMON
1	PHE0000002	5070	Arabidopsis AtHAP3a	Aldolase		
1	PHE0000002	163	Arabidopsis AtHAP3a	rice actin		PMON80861
2	PHE0000003	3	corn AtHAP3a -like1	rice actin		PMON80530
3	PHE0000004	4	corn AtHAP3a -like2	rice actin		PMON67819

SEQ ID NO	Phe ID	Nom ID	Gene Name	Promoter	Target	pMON
4	PHE0000005	5	corn AtHAP3a -like3	rice actin		PMON67820
5	PHE0000021	2715	Arabidopsis CCA1	Aldolase		
5	PHE0000021	2716	Arabidopsis CCA1	PPDK		
5	PHE0000021	31	Arabidopsis CCA1	rice actin		PMON80919
6	PHE0000041	72	corn hemoglobin 2	rice actin		
6	PHE0000041	75	corn hemoglobin 2	rice actin	chloroplast	
7	PHE0000066	140	At TOR1-like	rice actin		
8	PHE0000078	160	E. coli glnB	rice actin		PMON69471
8	PHE0000078	161	E. coli glnB	rice actin	chloroplast	PMON77877
9	PHE0000080	170	G28/BAA32418	rice actin		PMON68366
10	PHE0000081	171	G378	rice actin		PMON67814
11	PHE0000094	184	G464	rice actin		PMON68360
12	PHE0000112	202	Curly Leaf - variant 1	rice actin		
13	PHE0000113	203	Curly Leaf - variant 2	rice actin		PMON68365
14	PHE0000140	230	casein kinase II alpha subunit	rice actin		PMON73157
15	PHE0000151	241	adenosylhomocysteinase	rice actin		PMON67822
16	PHE0000199	292	ethylene response sensor	rice actin		PMON80534
16	PHE0000199	1086	ethylene response sensor	Z27		
17	PHE0000214	307	maize glycine rich protein	rice actin		
18	PHE0000364	455	wilt-like 1	rice actin		PMON77882
19	PHE0000365	456	wilt-like 2	rice actin		
20	PHE0000366	457	wilt-like 3	rice actin		
21	PHE0000367	458	wilt-like 4	rice actin		PMON72500
22	PHE0000372	463	G1073	rice actin		PMON72460
23	PHE0000373	464	G1411	rice actin		PMON73151
24	PHE0000374	465	G1449	rice actin		PMON73152
25	PHE0000375	466	G1635	rice actin		PMON73153
26	PHE0000376	467	G188	rice actin		PMON73154
27	PHE0000377	468	G19	rice actin		PMON73155
28	PHE0000378	469	G559	rice actin		PMON72461
29	PHE0000379	470	G865	rice actin		PMON72457
30	PHE0000381	4015	corn CCA1	Aldolase		
30	PHE0000381	4016	corn CCA1	PPDK		
30	PHE0000381	472	corn CCA1	rice actin		PMON72469
31	PHE0000383	146	700151210_FLI - corn L5 a	rice actin		
32	PHE0000384	473	LIB3957-023-C10_FLI - corn C-type cyclin	rice actin		PMON68621
33	PHE0000405	494	ASH2 - F17I14_190	rice actin		PMON81200
34	PHE0000406	495	soy ASH2-like 1	rice actin		PMON67841
35	PHE0000407	496	soy ASH2-like 3	rice actin		PMON67842
36	PHE0000408	497	soy ASH2-like 4	rice actin		
37	PHE0000409	498	corn pescadillo-like 1	rice actin		PMON72496
38	PHE0000410	499	yeast pescadillo homologue - Z72888	rice actin		PMON81718
39	PHE0000424	513	soy GA2-oxidase	rice actin		PMON80911
40	PHE0000447	536	corn phospholipase C 1	rice actin		

SEQ ID NO	Phe ID	Nom ID	Gene Name	Promoter	Target	pMON
41	PHE0000448	537	corn diacylglycerol kinase 2	rice actin		
42	PHE0000449	538	corn Ins(1,4,5)P(3) 5-phosphatase 1	rice actin		
43	PHE0000459	3371	Anabaena SPP	Glutelin1 3.1 kb		
43	PHE0000459	548	Anabaena SPP	rice actin		PMON68390
44	PHE0000460	549	Corn SPP	rice actin		PMON73751
45	PHE0000461	550	UDPgpp	rice actin		PMON67829
46	PHE0000464	553	soy U-box protein 1	rice actin		
47	PHE0000465	554	soy U-box protein 2	rice actin		
48	PHE0000466	555	soy U-box protein 3	rice actin		
49	PHE0000467	556	corn U-box protein 3	rice actin		PMON79434
50	PHE0000468	557	corn U-box protein 4	rice actin		
51	PHE0000474	563	yeast ado1	rice actin		PMON75469
52	PHE0000475	564	corn adenosine kinase 1	rice actin		PMON79437
53	PHE0000476	565	soy adenosine kinase 2	rice actin		PMON73773
54	PHE0000477	566	Synechocystis hypothetical sugar kinase - BAA10827	rice actin		PMON68401
55	PHE0000478	567	corn adenosylhomocysteinase 1	rice actin		
56	PHE0000479	568	yeast S-adenosyl-L-homocysteine hydrolase - NP_010961	rice actin		PMON68402
57	PHE0000480	569	Synechocystis S-adenosylhomocysteine hydrolase-BAA18079	rice actin		PMON75458
58	PHE0000481	570	soy RING finger protein 1 [BCRA1]	rice actin		PMON75472
59	PHE0000482	571	Aspergillus yA (laccase 1) - X52552	rice actin		
60	PHE0000483	3374	Synechocystis Sucrose phosphate synthase	Glutelin1 3.1 kb		
60	PHE0000483	572	Synechocystis Sucrose phosphate synthase	rice actin		
61	PHE0000487	576	yeast HAL3-Z28297	rice actin		PMON80267
62	PHE0000488	577	yeast GLC8-P41818	rice actin		PMON75473
63	PHE0000489	578	corn HAL3-like 1-LIB3060-046-G12_FLI	rice actin		PMON74432
64	PHE0000490	579	corn HAL3-like 2-	rice actin		
65	PHE0000491	580	corn GLC8-like 2	rice actin		PMON72489
66	PHE0000492	581	corn GLC8-like 1	rice actin		PMON69490
67	PHE0000493	582	Synechocystis ssr3189 - BAA17701	rice actin		PMON68403
67	PHE0000493	583	Synechocystis ssr3189 - BAA17701	rice actin	chloroplast	PMON75486
68	PHE0000494	584	Synechocystis ssr2315 - BAA17190	rice actin		PMON75459
68	PHE0000494	585	Synechocystis ssr2315 - BAA17190	rice actin	chloroplast	PMON75484
69	PHE0000495	586	Agrobacterium aiiA-like protein [attM] - AAD43990	rice actin		PMON73763
70	PHE0000496	587	Xylella aiiA-like protein -	rice actin		

SEQ ID NO	Phe ID	Nom ID	Gene Name	Promoter	Target	pMON
			XF1361			
71	PHE0000497	588	Xanthomonas aiiA - like protein	rice actin		
72	PHE0000498	589	corn histone H4	Z27		PMON76305
73	PHE0000499	590	high sulfur zein protein precursor	rice actin		PMON72490
73	PHE0000499	1082	high sulfur zein protein precursor	Z27		PMON77894
74	PHE0000500	591	corn RING finger protein 25	rice actin		PMON69495
74	PHE0000500	1415	corn RING finger protein 25	Z27		
75	PHE0000501	592	corn MKP 1 [MAP kinase 4]	rice actin		PMON69494
76	PHE0000502	593	corn MKP 3 [MAP kinase 5]	rice actin		PMON75474
77	PHE0000503	594	corn MKP 4	rice actin		PMON69493
78	PHE0000504	595	corn MKP 6	rice actin		
79	PHE0000505	596	corn MKP 7	rice actin		
80	PHE0000506	597	corn MKP 8 [cdc2 kinase]	rice actin		
81	PHE0000507	598	soy MKP 1	rice actin		PMON69492
82	PHE0000508	599	soy MKP 4	rice actin		PMON79438
83	PHE0000509	600	corn ABF2-like 1	rice actin		
84	PHE0000510	601	soy ABF2-like 1	rice actin		PMON72491
85	PHE0000511	2919	maize PPDK	PPDK		
85	PHE0000511	602	maize PPDK	rice actin		
86	PHE0000512	603	yeast YOR161c - Z75069	rice actin		PMON74444
86	PHE0000512	604	yeast YOR161c - Z75069	rice actin	chloroplast	PMON75489
87	PHE0000513	605	yeast HNM1 - Z72599	rice actin		PMON80268
87	PHE0000513	606	yeast HNM1 - Z72599	rice actin	chloroplast	PMON78908
88	PHE0000514	607	Xylella SAG13-like - E82748	rice actin		PMON76327
89	PHE0000515	608	corn SAG13-like 1	rice actin		PMON81211
90	PHE0000516	609	soy SAG13-like 1	rice actin		PMON72492
91	PHE0000517	610	soy SAG13-like 2	rice actin		PMON72493
92	PHE0000518	611	Nostoc punctiforme SAG13-like	rice actin		PMON75475
93	PHE0000520	613	corn clavata3-like	rice actin		PMON68609
94	PHE0000521	614	corn clavata3-like	rice actin		PMON69489
95	PHE0000522	615	wheat clv3-like	rice actin		PMON80941
96	PHE0000523	616	corn clv3-like 2	rice actin		PMON69487
97	PHE0000524	617	corn ESR2	rice actin		PMON69491
98	PHE0000525	618	corn violaxanthin de-epoxidase	rice actin		PMON75497
99	PHE0000526	619	rice serine acetyltransferase 1	rice actin		
100	PHE0000527	620	rice serine acetyltranferase 2	rice actin		PMON74446
101	PHE0000528	621	corn CEO-like protein	rice actin		PMON81282
102	PHE0000529	622	wheat nicotianamine aminotransferase	rice actin		PMON69482
103	PHE0000530	623	corn nicotianamine synthase 1	rice actin		PMON80946
104	PHE0000531	624	corn ys1-like1	rice actin		
105	PHE0000532	625	rice glutamate decarboxylase	rice actin		
106	PHE0000533	3862	rice GA2 oxidase	Aldolase		
106	PHE0000533	3863	rice GA2 oxidase	PPDK		
106	PHE0000533	626	rice GA2 oxidase	rice actin		PMON81274
107	PHE0000534	627	corn mlo-like 1	rice actin		

SEQ ID NO	Phe ID	Nom ID	Gene Name	Promoter	Target	pMON
108	PHE0000535	628	corn G alpha 1	rice actin		PMON68615
109	PHE0000536	629	corn G beta 2	rice actin		PMON74447
110	PHE0000537	630	corn g gamma-like 1	rice actin		
111	PHE0000538	631	rice tubby 1	rice actin		
112	PHE0000539	632	maize tubby 3	rice actin		PMON74448
113	PHE0000540	633	maize tubby 4	rice actin		PMON75451
114	PHE0000541	634	corn tubby 5	rice actin		PMON81245
115	PHE0000542	635	maize tubby 6	rice actin		PMON68613
116	PHE0000543	636	maize tubby 7	rice actin		PMON69499
117	PHE0000544	637	corn tubby 9	rice actin		PMON68616
118	PHE0000545	638	rice LRR.F-box protein 1	rice actin		
119	PHE0000546	639	corn LRR.F-box protein 7	rice actin		
120	PHE0000547	640	cotton ttg1-1	rice actin		PMON76304
121	PHE0000548	641	corn nucellin-like protein 1	rice actin		PMON75973
122	PHE0000549	642	rice nucellin-like protein 1	rice actin		PMON75974
123	PHE0000550	643	rice G1449-like 1	rice actin		PMON74449
124	PHE0000551	644	rice LEA 1	rice actin		PMON74450
125	PHE0000552	645	rice LEA 2 [wsi18]	rice actin		PMON75460
126	PHE0000553	646	corn LEA 1	rice actin		
127	PHE0000554	647	corn LEA 2	rice actin		
128	PHE0000555	649	corn adenylate transporter 1	Glutelin1 3.1 kb		
128	PHE0000555	648	corn adenylate transporter 1	rice actin		
129	PHE0000556	650	Xylella adenylate transporter - XF1738	rice actin	chloroplast	
130	PHE0000557	651	yeast AAC2 - Z35791	rice actin	chloroplast	PMON68638
131	PHE0000558	652	yeast TFS1 - X62105	rice actin		PMON68637
132	PHE0000559	653	yeast YLR179C-AAB67472	rice actin		PMON74431
133	PHE0000560	654	ZmSPS2-2	rice actin		PMON80524
134	PHE0000561	655	rice FPF1-like 1	rice actin		PMON68620
135	PHE0000562	656	rice FPF1-like 3	rice actin		PMON75303
136	PHE0000563	657	corn FPF1-like 1	rice actin		PMON80924
137	PHE0000564	658	corn FPF1-like 6	rice actin		PMON68619
138	PHE0000565	659	corn FLC-like 3	rice actin		PMON69483
139	PHE0000566	660	corn FLC-like 9	rice actin		PMON75304
140	PHE0000567	661	corn selenium-binding protein	rice actin		PMON81267
141	PHE0000568	662	maize glutathione S-transferase IV	rice actin		PMON69488
142	PHE0000569	663	calcium-dependent protein kinase	rice actin		
143	PHE0000570	664	protein kinase CK2 regulatory subunit CK2B3	rice actin		PMON76301
144	PHE0000571	665	19K zein precursor	rice actin		PMON69484
145	PHE0000572	666	corn EREBP/AP2-like transcription factor	rice actin		PMON75975
146	PHE0000573	667	G-box binding factor 1	rice actin		PMON68624
147	PHE0000574	668	corn high mobility group protein	rice actin		PMON74442
148	PHE0000575	669	corn glycine-rich RNA-binding protein	rice actin		

SEQ ID NO	Phe ID	Nom ID	Gene Name	Promoter	Target	pMON
149	PHE0000576	670	corn enolase 1	rice actin		PMON75452
150	PHE0000577	671	maize RING finger protein	rice actin		PMON81277
151	PHE0000578	672	maize 60S acidic ribosomal protein P0	rice actin		PMON69485
152	PHE0000579	673	corn nucleotide-binding protein	rice actin		PMON68623
153	PHE0000580	674	MADS affecting flowering 1-AAK37527	rice actin		PMON68611
154	PHE0000581	675	G1760 - Q9SZJ6	rice actin		PMON68612
155	PHE0000582	676	G2010 - CAB56582	rice actin		PMON75476
156	PHE0000583	677	SAG13 - AAF09487	rice actin		PMON80926
157	PHE0000584	678	Rice SAG13-like	rice actin		PMON68610
158	PHE0000585	679	corn FLT-like 1	rice actin		PMON68622
159	PHE0000586	680	corn FLT-like 2	rice actin		PMON68618
160	PHE0000587	681	corn FLT-like 3	rice actin		PMON80928
161	PHE0000588	682	rice leafy - AB005620	rice actin		
162	PHE0000589	683	corn HD1-like 1	rice actin		PMON80942
163	PHE0000590	685	rice plastidic ATP/ADP-transporter - BAB40979	Glutelin1 3.1 kb		
163	PHE0000590	684	rice plastidic ATP/ADP-transporter - BAB40979	rice actin		
164	PHE0000591	687	rice L5 a	rice actin		PMON68633
165	PHE0000592	688	corn L5	rice actin		PMON68639
166	PHE0000593	689	corn L5-like	rice actin		PMON68634
167	PHE0000594	690	Agrobacterium ornithine decarboxylase	rice actin		PMON75496
168	PHE0000601	697	corn IAP-like RING finger protein 1	rice actin		
169	PHE0000602	698	yeast BIR1	rice actin		PMON80537
170	PHE0000603	699	corn BAX inhibitor 1-like 1	rice actin		PMON68626
171	PHE0000604	700	corn Bax inhibitor 1-like 2	rice actin		PMON68625
172	PHE0000605	701	corn Bax inhibitor 1-like 3	rice actin		
173	PHE0000606	702	corn caspase-like 1	rice actin		PMON80938
174	PHE0000607	703	corn caspase-like 2	rice actin		
175	PHE0000608	704	corn caspase-like 3	rice actin		PMON68404
176	PHE0000609	705	yeast YOR197w	rice actin		PMON74443
177	PHE0000610	706	soy Lls1-like	rice actin		PMON75494
178	PHE0000611	707	Synechocystis Rieske iron-sulfur protein	rice actin		PMON68405
178	PHE0000611	708	Synechocystis Rieske iron-sulfur protein	rice actin	chloroplast	PMON75483
179	PHE0000612	709	Arabidopsis AGL15	rice actin		
180	PHE0000613	710	yeast OST2	rice actin		PMON80511
181	PHE0000614	711	corn DAD1	rice actin		PMON68632
182	PHE0000615	712	corn pirin	rice actin		PMON80943
183	PHE0000616	713	corn betaine-aldehyde dehydrogenase	rice actin		
184	PHE0000617	714	rice betaine aldehyde dehydrogenase	rice actin		

SEQ ID NO	Phe ID	Nom ID	Gene Name	Promoter	Target	pMON
185	PHE0000618	715	yeast PEM1/CHO2	rice actin		PMON80520
186	PHE0000619	716	yeast PEM2/OPI3	rice actin		PMON74435
187	PHE0000620	717	corn phosphoethanolamine N-methyltransferase 2	rice actin		PMON75495
188	PHE0000621	718	E. coli betT	rice actin		PMON75482
188	PHE0000621	719	E. coli betT	rice actin	chloroplast	PMON73769
189	PHE0000622	720	Xenorhabdus BetT-like 1	rice actin		PMON81892
189	PHE0000622	721	Xenorhabdus BetT-like 1	rice actin	chloroplast	
190	PHE0000623	722	corn NHX1-like 1	rice actin		PMON74438
191	PHE0000624	723	OsNHX1 - AB021878	rice actin		PMON80857
192	PHE0000625	724	corn vacuolar H+-pyrophosphatase 1	rice actin		PMON74445
193	PHE0000626	725	corn vacuolar H+-pyrophosphatase 2	rice actin		PMON68406
194	PHE0000627	726	corn vacuolar H+-pyrophosphatase 5	rice actin		
195	PHE0000628	727	soy homeobox-leucine zipper protein homolog h1-	rice actin		
196	PHE0000629	728	soy zinc finger protein	rice actin		PMON68631
197	PHE0000630	729	soy TGACG-motif-binding protein STF2	rice actin		PMON68648
198	PHE0000631	730	corn putative zinc finger protein	rice actin		PMON75454
199	PHE0000632	731	soy AP2 domain transcription factor	rice actin		PMON68635
200	PHE0000633	732	soy pseudo-response regulator	rice actin		PMON74439
201	PHE0000634	733	soy CONSTANS-like B-box zinc finger protein	rice actin		PMON74436
202	PHE0000635	734	soy RPT2-like	rice actin		PMON68407
203	PHE0000636	735	corn myb-related protein	rice actin		PMON76302
204	PHE0000637	736	Arabidopsis salt-tolerance protein	rice actin		PMON75455
205	PHE0000638	737	soy AP2 domain transcription factor	rice actin		PMON75456
206	PHE0000639	738	soy late elongated hypocotyl	rice actin		PMON75457
207	PHE0000640	739	soy zinc finger protein	rice actin		PMON74440
208	PHE0000641	740	soy putative protein kinase	rice actin		
209	PHE0000642	741	soy auxin-responsive GH3 protein	rice actin		
210	PHE0000643	742	corn ripening-related protein	rice actin		
211	PHE0000644	743	corn beta-expansin 4	rice actin		
212	PHE0000645	744	corn hypothetical protein	rice actin		PMON68640
213	PHE0000646	745	corn unknown protein	rice actin		PMON80348
214	PHE0000647	746	corn unknown protein	rice actin		PMON74437
215	PHE0000648	747	corn unknown protein	rice actin		PMON74441
216	PHE0000649	748	soy unknown protein	rice actin		PMON78901
217	PHE0000650	749	corn unknown protein	rice actin		PMON76303
218	PHE0000651	750	rice Lls1 (CAO) - AF284781	rice actin		PMON80339
219	PHE0000654	754	G896	rice actin		PMON68605
220	PHE0000655	3951	G1435	Aldolase		

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220	PHE0000655	3952	G1435	PPDK		
220	PHE0000655	755	G1435	rice actin		PMON68607
221	PHE0000656	3953	LIB4074-003-H1_FLI - corn G1435-like	Aldolase		
221	PHE0000656	3954	LIB4074-003-H1_FLI - corn G1435-like	PPDK		
221	PHE0000656	756	LIB4074-003-H1_FLI - corn G1435-like	rice actin		PMON80923
222	PHE0000658	759	G1496	Barley Per1		
222	PHE0000658	758	G1496	rice actin		PMON68606
223	PHE0000660	761	700072387_FLI - ZmSPS3-1	rice actin		PMON80533
224	PHE0000661	762	GATE90 - ZmSPS2-3	rice actin		
225	PHE0000662	763	corn ELI17-like protein 1	rice actin		PMON80944
226	PHE0000663	764	soy ELI17-like protein 1	rice actin		
227	PHE0000664	768	X58872 - E. coli hmp1	rice actin		PMON80257
227	PHE0000664	769	X58872 - E. coli hmp1	rice actin	chloroplast	PMON80257
228	PHE0000665	765	Nostoc sp. PCC 7120 glnB	rice actin		PMON80261
228	PHE0000665	766	Nostoc sp. PCC 7120 glnB	rice actin	chloroplast	
229	PHE0000666	767	Brassica P-II	rice actin		PMON68398
230	PHE0000700	93	pMON57278 - Arabidopsis eskimo 1	rice actin		PMON81677
231	PHE0000701	774	soy 1-deoxy-D-xylulose-5-phosphate reductoisomerase-	Barley Per1		
231	PHE0000701	773	soy 1-deoxy-D-xylulose-5-phosphate reductoisomerase-	rice actin		PMON79439
232	PHE0000702	775	Synechocystis 1-deoxy-D-xylulose-5-phosphate reductoisomerase-D64000	rice actin	chloroplast	PMON77883
233	PHE0000703	776	Agrobacterium 1-deoxy-D-xylulose 5-phosphate reductoisomerase-AAK88334	rice actin	chloroplast	PMON75517
234	PHE0000704	778	corn 1-deoxy-D-xylulose-5-phosphate synthase-	Barley Per1		
234	PHE0000704	777	corn 1-deoxy-D-xylulose-5-phosphate synthase-	rice actin		PMON76315
235	PHE0000705	779	Agrobacterium 1-deoxy-D-xylulose-5-phosphate synthase-AAK86554	rice actin	chloroplast	PMON75516
236	PHE0000706	780	Xylella 1-deoxyxylulose-5-phosphate synthase-AAF85048	rice actin	chloroplast	
237	PHE0000709	783	corn HMT 1	rice actin		PMON68643
238	PHE0000710	784	corn HMT 2	rice actin		PMON80343
239	PHE0000711	785	E. coli yagD homocysteine S-methyltransferase-Q47690	rice actin		PMON73752
240	PHE0000712	786	yeast Mht1 - NP_013038	rice actin		PMON73753
241	PHE0000713	787	corn H2A.F/Z 1	rice actin		
242	PHE0000714	788	corn H2A 1	rice actin		PMON68642
243	PHE0000715	789	corn H2A 3	rice actin		PMON68641
244	PHE0000716	790	corn H2A 7	rice actin		PMON68644

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245	PHE0000717	15	wilt-1256	rice actin		
245	PHE0000717	16	Antisense wilt-1256	rice actin		
246	PHE0000735	808	corn NAD(P)H quinone oxidoreductase	rice actin		PMON75481
247	PHE0000736	809	rice CBP80 - AY017415	rice actin		
248	PHE0000737	810	yeast GCR3 - D10224	rice actin		PMON12345
249	PHE0000738	811	corn CBP20	rice actin		PMON12346
250	PHE0000739	812	yeast CBC2 - Z73534	rice actin		PMON12347
251	PHE0000740	813	rice serine decarboxylase - AAG12476	rice actin		PMON12348
252	PHE0000741	814	corn serine decarboxylase	rice actin		PMON12349
253	PHE0000742	815	soy serine decarboxylase	rice actin		PMON75478
254	PHE0000743	816	yeast DBF2 - P22204	rice actin		PMON81215
255	PHE0000744	817	yeast DBF20 - P32328	rice actin		PMON76330
256	PHE0000745	818	Arabidopsis agl8 - Q38876	rice actin		PMON73776
257	PHE0000746	819	corn AGL8-like B	rice actin		PMON73777
258	PHE0000747	820	corn PHR1-like 1	rice actin		PMON75480
259	PHE0000748	821	corn PHR1-like 2	rice actin		PMON75479
260	PHE0000749	822	Nitrosomonas europaea dual function SBPase/FBPase-	rice actin	chloroplast	
261	PHE0000750	823	rice VP14-like 1	rice actin		
262	PHE0000751	824	rice VP14-like 2	rice actin		PMON75321
263	PHE0000754	827	rice ANT-like	rice actin		PMON73762
264	PHE0000755	828	Nostoc sp. PCC 7120 GlpX protein	rice actin	chloroplast	PMON80513
265	PHE0000756	829	Nostoc punctiforme strain ATCC 29133 GlpX protein-NOS1c0617	rice actin	chloroplast	PMON77884
266	PHE0000757	830	Anabaena SPS C154	rice actin		PMON68649
267	PHE0000758	831	Anabaena SPS C287	rice actin		PMON75951
268	PHE0000762	835	G557 (HY5)	rice actin		PMON75464
269	PHE0000763	836	G189	rice actin		PMON75956
270	PHE0000764	837	G736	rice actin		PMON75465
271	PHE0000765	838	G1073	rice actin		
272	PHE0000766	839	G671	rice actin		PMON75466
273	PHE0000767	840	G247	rice actin		PMON75952
274	PHE0000768	841	G1384	rice actin		PMON75467
275	PHE0000769	842	G779	rice actin		PMON75960
276	PHE0000770	843	G1795	rice actin		PMON75954
277	PHE0000771	844	G977	rice actin		PMON81285
278	PHE0000772	845	G568	rice actin		PMON75468
279	PHE0000773	846	G1269	rice actin		PMON81772
280	PHE0000774	847	G1050	rice actin		PMON75461
281	PHE0000779	852	yeast GPA2	rice actin		PMON76307
282	PHE0000796	869	phytosulfokine 4 - 13399211	rice actin		PMON75330
283	PHE0000797	870	rice phytosulfokine 2 - 13399209	rice actin		PMON75322
284	PHE0000798	871	rice phytosulfokine-alpha - 11907498	rice actin		PMON80485

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285	PHE0000799	872	rice phytosulphokine SH27A - 3201971	rice actin		PMON75317
286	PHE0000800	873	AtSUC1	rice actin		PMON81820
287	PHE0000801	874	Arabidopsis SUT2	rice actin		PMON75529
288	PHE0000802	875	Arabidopsis SUT4	rice actin		PMON76337
289	PHE0000803	876	OsSUT1 - D87819	rice actin		
290	PHE0000804	877	OsSUT3 - AB071809	rice actin		PMON81272
291	PHE0000805	878	Aspergillis phytochrome	rice actin		PMON77898
292	PHE0000806	881	corn histidine phosphotransfer protein 1	rice actin		PMON76308
293	PHE0000807	882	corn histidine phosphotransfer protein 2	rice actin		PMON76309
294	PHE0000808	883	soy histidine phosphotransfer protein 1	rice actin		PMON76310
295	PHE0000809	884	YPD1 - Z74283	rice actin		PMON76311
296	PHE0000810	885	rice ethylene receptor - AF013979	rice actin		PMON75319
297	PHE0000811	886	rice ethylene responsive factor - AAK70909	rice actin		
298	PHE0000812	887	CYP79F1 (supershoot) - AF370512	rice actin		
299	PHE0000813	888	AtSUC2	rice actin		PMON75530
300	PHE0000814	889	soy G28 like	rice actin		PMON77897
301	PHE0000815	890	corn G1792-like 2	rice actin		PMON73841
302	PHE0000816	891	G1792	rice actin		PMON76312
303	PHE0000817	892	corn duf6 2	rice actin		
304	PHE0000818	893	corn duf6 3	rice actin		
305	PHE0000819	894	corn duf6	rice actin		PMON75324
306	PHE0000820	895	corn duf6 6	rice actin		PMON81721
307	PHE0000822	897	corn duf6 11	rice actin		PMON73799
308	PHE0000823	898	corn duf6 12	rice actin		PMON75325
309	PHE0000824	899	corn duf6 13	rice actin		
310	PHE0000825	900	corn duf6 14	rice actin		PMON77892
311	PHE0000826	901	corn duf6 15	rice actin		PMON75342
312	PHE0000827	902	corn duf6 16	rice actin		PMON75326
313	PHE0000828	903	corn duf6 17	rice actin		PMON75327
314	PHE0000829	904	corn duf6 18	rice actin		PMON73800
315	PHE0000830	905	corn duf6 19	rice actin		PMON73801
316	PHE0000831	906	corn duf6 20	rice actin		PMON76331
317	PHE0000832	907	soy duf6 1	rice actin		PMON75343
318	PHE0000833	908	soy duf6 2	rice actin		PMON77854
319	PHE0000834	909	soy duf6 3	rice actin		PMON76316
320	PHE0000835	910	soy duf6 4	rice actin		PMON75344
321	PHE0000836	911	soy duf6 5	rice actin		PMON75328
322	PHE0000837	912	soy duf6 6	rice actin		PMON77863
323	PHE0000838	913	soy duf6 7	rice actin		PMON73802
324	PHE0000839	914	soy duf6 8	rice actin		PMON73803

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325	PHE0000840	915	soy duf6 9	rice actin		PMON81781
326	PHE0000841	916	soy duf6 10	rice actin		PMON75345
327	PHE0000842	917	soy duf6 11	rice actin		PMON75329
328	PHE0000843	918	soy duf6 12	rice actin		PMON75346
329	PHE0000844	919	soy duf6 13	rice actin		PMON73794
330	PHE0000845	920	soy duf6 15	rice actin		PMON76313
331	PHE0000846	922	rice Crinkly4 - AB057787	Glutelin1 3.1 kb		
331	PHE0000846	921	rice Crinkly4 - AB057787	rice actin		
332	PHE0000847	924	rice S-domain receptor-like protein kinase 1-BAA94516	Glutelin1 3.1 kb		
332	PHE0000847	923	rice S-domain receptor-like protein kinase 1-BAA94516	rice actin		
333	PHE0000848	926	rice S-domain receptor-like protein kinase 2 - BAB07906.1	Glutelin1 3.1 kb		
333	PHE0000848	925	rice S-domain receptor-like protein kinase 2 - BAB07906.1	rice actin		
334	PHE0000849	927	rice S-domain receptor-like protein kinase 3 - BAB07905.1	rice actin		PMON80287
334	PHE0000849	928	rice S-domain receptor-like protein kinase 3 - BAB07905.1	Z27		
335	PHE0000850	930	rice S-domain receptor-like protein kinase 4 - BAB07904.1	Glutelin1 3.1 kb		
335	PHE0000850	929	rice S-domain receptor-like protein kinase 4 - BAB07904.1	rice actin		
336	PHE0000851	932	rice S-domain receptor-like protein kinase 5	Glutelin1 3.1 kb		
336	PHE0000851	931	rice S-domain receptor-like protein kinase 5	rice actin		
337	PHE0000852	934	rice S-receptor kinase PK3 - BAB64641.1	Glutelin1 3.1 kb		
337	PHE0000852	933	rice S-receptor kinase PK3 - BAB64641.1	rice actin		
338	PHE0000853	935	OsPK10 - L27821	rice actin		PMON75332
338	PHE0000853	936	OsPK10 - L27821	Z27		PMON77893
339	PHE0000854	937	soy 14-3-3 22	rice actin		PMON73795
340	PHE0000855	938	soy 14-3-3 22 N-terminus	rice actin		PMON75347
341	PHE0000856	939	14-3-3-like protein N-terminus	rice actin		PMON73796
342	PHE0000857	940	sorghum 14-3-3 10	rice actin		PMON75348
343	PHE0000858	941	sorghum 14-3-3 10 N-terminus	rice actin		PMON73797
344	PHE0000859	942	rice 14-3-3 15	rice actin		PMON73798
345	PHE0000860	943	rice 14-3-3 15 N-terminus	rice actin		PMON75333
346	PHE0000861	944	corn 14-3-3 13	rice actin		PMON75334
347	PHE0000862	945	corn 14-3-3 13 N-terminus	rice actin		PMON75335
348	PHE0000863	946	14-3-3 protein N-terminus	rice actin		PMON75349
349	PHE0000864	947	rice 14-3-3 10	rice actin		PMON75350
350	PHE0000865	948	rice 14-3-3 10 N-terminus	rice actin		PMON75336
351	PHE0000866	949	soy 14-3-3 21	rice actin		PMON77851
352	PHE0000867	950	soy 14-3-3 21 N-terminus	rice actin		PMON75337
353	PHE0000868	951	wheat 14-3-3 10	rice actin		PMON75338

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354	PHE0000869	952	wheat 14-3-3 10 N-terminus	rice actin		PMON75339
355	PHE0000870	953	corn 14-3-3 17	rice actin		PMON75340
356	PHE0000871	954	corn 14-3-3 17 N-terminus	rice actin		PMON75341
357	PHE0000872	955	rice G alpha XL - BAA93022	rice actin		
358	PHE0000873	956	yeast casein kinase II alpha - CAA86916	rice actin		PMON79671
359	PHE0000874	957	rice casein kinase alpha subunit - AAL34126	rice actin		
360	PHE0000875	958	soy casein kinase alpha	rice actin		
361	PHE0000876	959	rice casein kinase II beta subunit - AAG60201	rice actin		PMON75323
362	PHE0000877	960	yeast CKB1 - Z72541	rice actin		
363	PHE0000878	961	corn casein kinase beta 1	rice actin		PMON77852
364	PHE0000879	962	corn casein kinase beta 2	rice actin		
365	PHE0000884	967	CAR1-like 1	rice actin		
366	PHE0000885	968	corn CAR1-like 3	rice actin		PMON77853
367	PHE0000886	969	corn CAR1-like 4	rice actin		PMON73804
368	PHE0000887	970	corn CAR1-like 5	rice actin		PMON73805
369	PHE0000888	971	yeast hnRNP methyltransferase-CAA53689	rice actin		PMON73830
370	PHE0000889	972	corn arginine N-methyl transferase 1	rice actin		
371	PHE0000890	973	corn arginine N-methyl transferase 2	rice actin		PMON82191
372	PHE0000891	974	CAR1 - corn ABA inducible RNA-binding protein	rice actin		
373	PHE0000892	975	corn RING finger 100	rice actin		PMON77864
374	PHE0000893	976	corn RING finger 101	rice actin		PMON73831
375	PHE0000894	977	corn RING finger 103	rice actin		PMON73832
376	PHE0000895	978	corn RING finger 102	rice actin		
377	PHE0000896	979	corn RING finger 104	rice actin		
378	PHE0000897	980	corn RING finger 105	rice actin		PMON73833
379	PHE0000898	981	corn RING finger 106	rice actin		PMON81698
380	PHE0000899	982	corn RING finger 108	rice actin		
381	PHE0000900	983	corn RING finger 109	rice actin		
382	PHE0000901	984	corn RING finger 110 [ReMembR-H2 protein JR702]-	rice actin		
383	PHE0000902	985	corn RING finger 111	rice actin		
384	PHE0000903	986	corn RING finger 112	rice actin		PMON77865
385	PHE0000904	987	corn RING finger 113	rice actin		PMON81725
386	PHE0000905	988	corn RING finger 114	rice actin		PMON77866
387	PHE0000906	989	corn RING finger 115	rice actin		PMON73842
388	PHE0000907	990	corn RING finger 116	rice actin		PMON73843
389	PHE0000908	991	corn Skp1-like 118 [UIP2]	rice actin		PMON73844
390	PHE0000909	992	corn Skp1-like 119	rice actin		PMON73845
391	PHE0000910	993	corn Skp1-like 120 [UIP2]	rice actin		PMON73846
392	PHE0000911	994	corn F-box 123	rice actin		
393	PHE0000912	995	corn F-box 124 [TIR1]	rice actin		

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394	PHE0000913	996	corn F-box 125 [TIR1]	rice actin		PMON78201
395	PHE0000914	997	corn F-box 126	rice actin		
396	PHE0000915	998	corn RING finger 128 [response regulator 6]	rice actin		
397	PHE0000916	999	corn RING finger 132	rice actin		PMON73847
398	PHE0000917	1000	corn RING finger 133	rice actin		PMON81797
399	PHE0000918	1001	corn ASH1	rice actin		PMON76338
400	PHE0000919	1002	corn RING finger 136	rice actin		PMON73848
401	PHE0000920	1003	corn RING finger 138	rice actin		
402	PHE0000921	1004	corn F-box 141	rice actin		
403	PHE0000922	1005	corn F-box 142	rice actin		
404	PHE0000923	1006	corn F-box 143	rice actin		PMON73834
405	PHE0000924	1007	corn F-box 144	rice actin		
406	PHE0000925	1008	corn F-box 145	rice actin		PMON73835
407	PHE0000926	1009	corn RING finger 147	rice actin		
408	PHE0000927	1010	corn RING finger 149 [anaphase promoting complex subunit 11]-	rice actin		
409	PHE0000928	1011	corn RING finger 151 [ROC1]	rice actin		PMON77868
410	PHE0000929	1012	corn U-box 153	rice actin		
411	PHE0000930	1013	corn RING finger 154 [VIP2]	rice actin		PMON73836
412	PHE0000931	1014	corn RING finger 155 [VIP2]	rice actin		
413	PHE0000932	1015	rice U-box 100	rice actin		
414	PHE0000933	1016	corn RING finger protein 157	rice actin		PMON73837
415	PHE0000934	1017	corn F-box 159 [FKF1-like]	rice actin		PMON78202
416	PHE0000935	1018	corn F-box 160 [FKF-like]	rice actin		
417	PHE0000936	1019	corn RING finger 161 [cellulose synthase]	rice actin		
418	PHE0000937	1020	corn RING finger 162 [cellulose synthase]	rice actin		
419	PHE0000938	1021	corn RING finger 163	rice actin		
420	PHE0000939	1022	corn RING finger 164	rice actin		PMON73838
421	PHE0000940	1023	corn RING finger 165	rice actin		PMON76317
422	PHE0000941	1024	corn F-box 166	rice actin		
423	PHE0000942	1025	corn RING finger 167 [seven in absentia-like]	rice actin		PMON76318
424	PHE0000943	1026	corn F-box 168	rice actin		
425	PHE0000944	1027	corn RING finger 169 [S-ribonuclease binding protein]	rice actin		PMON76319
426	PHE0000945	1028	corn F-box 170	rice actin		PMON76320
427	PHE0000946	1029	corn F-box 172	rice actin		
428	PHE0000947	1030	corn RING finger 174	rice actin		PMON75493
429	PHE0000948	1031	corn RING 175	rice actin		
430	PHE0000949	1032	corn Cullin 176	rice actin		PMON76321
431	PHE0000950	1033	corn RING finger 177	rice actin		
432	PHE0000951	1034	corn RING finger 178	rice actin		
433	PHE0000952	1035	corn RING finger 179 [alpha-galactosidase]	rice actin		

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434	PHE0000953	1036	corn RING finger 180	rice actin		PMON76322
435	PHE0000954	1037	corn F-box 181	rice actin		PMON76323
436	PHE0000955	1038	corn RING finger 182	rice actin		PMON76324
437	PHE0000956	1039	corn RING finger 183	rice actin		
438	PHE0000957	1040	corn RING finger 185	rice actin		PMON76325
439	PHE0000958	1041	corn F-box 186	rice actin		
440	PHE0000959	1042	corn F-box 187	rice actin		
441	PHE0000960	1043	corn RING/U-box 188	rice actin		
442	PHE0000961	1044	corn SPS2-4	rice actin		PMON80523
443	PHE0000962	1045	rice IRE1 - AB031396	rice actin		PMON80299
443	PHE0000962	1046	rice IRE1 - AB031396	Z27		
444	PHE0000963	1048	rice IRE1 N-terminal domain - AB031396	Glutelin1 3.1 kb		
444	PHE0000963	1047	rice IRE1 N-terminal domain - AB031396	rice actin		PMON80852
445	PHE0000964	1049	rice IRE1 C-terminal domain - AB031396	rice actin		PMON77867
445	PHE0000964	1050	rice IRE1 C-terminal domain - AB031396	Z27		PMON76349
446	PHE0000965	1052	yeast IRE1 - P32361	Glutelin1 3.1 kb		
446	PHE0000965	1051	yeast IRE1 - P32361	rice actin		
447	PHE0000966	1054	yeast IRE1 N-terminal domain - P32361	Glutelin1 3.1 kb		
447	PHE0000966	1053	yeast IRE1 N-terminal domain - P32361	rice actin		PMON79157
448	PHE0000967	1055	yeast IRE1 C-terminal domain - P32361	rice actin		PMON79158
448	PHE0000967	1056	yeast IRE1 C-terminal domain - P32361	Z27		PMON75538
449	PHE0000968	1057	corn cytosine deaminase-like	rice actin		
450	PHE0000969	1058	corn aldose reductase	rice actin		
451	PHE0000970	1059	soy NADPH dependent mannose 6-phosphate reductase-	rice actin		
452	PHE0000971	1060	yeast YBL107c - Z35868	rice actin		PMON73806
453	PHE0000972	1061	yeast Ydr210w - NP_010496	rice actin		PMON73807
454	PHE0000973	1062	yeast YDR209c - S61572	rice actin		PMON73827
455	PHE0000974	1063	yeast Soh1 - NP_011388	rice actin		PMON77855
456	PHE0000975	1064	yeast TAD2 - NP_012499	rice actin		PMON81203
457	PHE0000976	1065	yeast Yet1 - NP_012858	rice actin		PMON78912
458	PHE0000977	1066	yeast Ylr162w - NP_013263	rice actin		PMON80504
459	PHE0000978	1067	yeast Ynl010w - NP_014388	rice actin		PMON77856
460	PHE0000979	1068	yeast Ynl124w - NP_014275	rice actin		PMON73849
461	PHE0000980	1069	yeast Ydl124w - NP_010159	rice actin		PMON77869
462	PHE0000981	1070	yeast Ygr039w - NP_011553	rice actin		PMON77857
463	PHE0000982	1071	yeast Usa1 - NP_013683	rice actin		PMON80308
464	PHE0000983	1072	yeast Ynr061c - NP_014459	rice actin		PMON73808
465	PHE0000984	1073	yeast Glutaredoxin - NP_009895	rice actin		PMON73809
466	PHE0000985	1074	soy unknown protein	rice actin		

SEQ ID NO	Phe ID	Nom ID	Gene Name	Promoter	Target	pMON
467	PHE0000986	1075	soy putative protein	rice actin		PMON80929
468	PHE0000987	1076	corn CLC1	rice actin		PMON81774
469	PHE0000988	1077	corn CLD1	rice actin		PMON73810
470	PHE0000989	1078	rice Asr1 - AF039573	rice actin		PMON80515
471	PHE0000990	1079	rice CLC1-like 1 - BAB19059	rice actin		PMON77858
472	PHE0000991	1080	corn Asr1-like 1	rice actin		
473	PHE0000992	1081	corn Asr1-like 5	rice actin		PMON82170
474	PHE0000993	1083	corn sigma factor 1	rice actin		
475	PHE0000994	1084	corn sigma factor 2 [Sig3]	rice actin		PMON77870
476	PHE0000995	1085	corn sigma factor 3 [Sig1]	rice actin		PMON77871
477	PHE0000996	1087	corn bromodomain protein	rice actin		
478	PHE0000997	1088	corn homeodomain leucine zipper protein	rice actin		
479	PHE0000998	1089	corn bZIP protein 3	rice actin		PMON73811
480	PHE0000999	1090	corn bZIP protein 4 [G-box binding factor 1]	rice actin		
481	PHE0001000	1091	corn remorin like DNA-binding protein 1	rice actin		
482	PHE0001001	1092	corn remorin like DNA-binding protein 2	rice actin		PMON77859
483	PHE0001002	1093	corn Gld-Tea protein 2	rice actin		PMON73812
484	PHE0001003	1094	corn homeobox protein 1	rice actin		PMON73813
485	PHE0001004	1095	corn homeobox protein 3	rice actin		PMON77860
486	PHE0001005	1096	corn heat shock transcription factor 1	rice actin		
487	PHE0001006	1097	corn heat shock transcription factor 2	rice actin		PMON73814
488	PHE0001007	1098	corn heat shock transcription factor 3	rice actin		PMON80337
489	PHE0001008	1099	corn heat shock transcription factor 4	rice actin		
490	PHE0001009	1100	corn IAA-like 1	rice actin		
491	PHE0001010	1101	corn IAA-like 4	rice actin		
492	PHE0001011	1102	corn MADS box protein 100	rice actin		
493	PHE0001012	1103	corn MADS box protein 102	rice actin		
494	PHE0001013	1104	corn MADS box protein 103	rice actin		
495	PHE0001014	1105	corn MADS box protein 104	rice actin		PMON79159
496	PHE0001015	1106	corn MADS box protein 105	rice actin		
497	PHE0001016	1107	corn MADS box protein 108	rice actin		PMON73815
498	PHE0001018	1109	corn MADS box protein 114	rice actin		
499	PHE0001019	1110	corn LIM domain protein 1	rice actin		PMON73817
500	PHE0001020	1111	corn LIM domain protein 2	rice actin		PMON73818
501	PHE0001021	1112	corn myb-like DNA binding protein	rice actin		PMON73819
502	PHE0001022	1113	corn myb domain protein 1	rice actin		PMON73820
503	PHE0001023	1114	corn myb domain protein 3	rice actin		
504	PHE0001024	1115	corn myb domain protein 4	rice actin		
505	PHE0001025	1116	corn NAM-like protein	rice actin		PMON78203

SEQ ID NO	Phe ID	Nom ID	Gene Name	Promoter	Target	pMON
506	PHE0001026	1117	corn transcriptional co-activator-like protein 1	rice actin		PMON73821
507	PHE0001027	1118	corn LSD1-like protein 1	rice actin		PMON73822
509	PHE0001029	1120	corn RING finger 200	rice actin		PMON78913
510	PHE0001030	1121	corn RING finger protein 202	rice actin		PMON73824
511	PHE0001031	1122	corn PGPD14-like protein	rice actin		
512	PHE0001032	1123	corn Ankyrin protein 1	rice actin		PMON75528
513	PHE0001033	1124	corn zinc finger protein 10 [corn G325-like 3]	rice actin		PMON77861
514	PHE0001034	1125	corn scarecrow protein 100	rice actin		PMON77885
515	PHE0001035	1126	corn transcription elongation factor	rice actin		PMON73850
516	PHE0001036	1127	corn constans-like protein 10	rice actin		PMON80933
517	PHE0001037	1128	corn copine-like protein 1	rice actin		
518	PHE0001038	1129	corn copine-like protein 2	rice actin		PMON73839
519	PHE0001039	1130	corn RING finger protein 201	rice actin		PMON77862
520	PHE0001040	1131	corn zinc finger protein	rice actin		PMON73825
521	PHE0001041	1132	corn IAA-like 10	rice actin		
522	PHE0001042	1133	corn constans-like 5	rice actin		PMON73826
523	PHE0001043	367	soy G-gamma subunit DC-terminus	rice actin		PMON77881
524	PHE0001044	1134	soy AGL8-like 1	rice actin		PMON77876
525	PHE0001045	1135	soy AGL8-like 3	rice actin		PMON77872
526	PHE0001046	1136	corn Agl8D (LIB5131-001-H1)	rice actin		PMON80505
527	PHE0001047	1137	corn Agl8E (LIB5131-001-H2)	rice actin		PMON75318
528	PHE0001028	1119	corn GS1-like protein	rice actin		PMON73823
528	PHE0001048	1138	corn Agl8F (LIB5131-001-H3)	rice actin		PMON80862
529	PHE0001050	1140	Arabidopsis LFY	rice actin		PMON73780
530	PHE0001103	1193	corn Isr	rice actin		PMON77874
531	PHE0001104	1194	soy Isr-like 1	rice actin		PMON77875
532	PHE0001105	1195	rice Isr-like 1	rice actin		PMON81778
533	PHE0001160	1250	soy G1792-like	rice actin		PMON78914
534	PHE0001161	1251	corn sucrose export defective 1 (sdx1) - AF302187	rice actin		PMON80319
535	PHE0001162	1252	rice sdx1 delta ctp	rice actin	chloroplast	
536	PHE0001163	1253	Arabidopsis sucrose export defective 1-AF302188	rice actin		
537	PHE0001164	1254	Nostoc sp. PCC 7120 sdx1-like - 17134979	rice actin	chloroplast	
538	PHE0001165	1255	Synechocystis sp. PCC 6803 sdx1-like - 1652844	rice actin	chloroplast	PMON75513
539	PHE0001166	1256	Nostoc punctiforme sdx1-like	rice actin	chloroplast	PMON75514
540	PHE0001173	1263	corn CVY-CIK	rice actin		PMON80469
541	PHE0001187	1277	corn spa1-like	rice actin		
542	PHE0001188	1278	corn calcium dependant protein kinase	rice actin		
543	PHE0001189	1279	corn unknown protein	rice actin		
544	PHE0001190	1280	corn putative splicing factor	rice actin		PMON76340

SEQ ID NO	Phe ID	Nom ID	Gene Name	Promoter	Target	pMON
545	PHE0001191	1281	rice hydroxyproline-rich glycoprotein	rice actin		PMON80345
546	PHE0001192	1282	rice unknown protein - AAK14418	rice actin		
547	PHE0001193	1283	corn unknown protein	rice actin		PMON75522
548	PHE0001194	1284	corn alpha-amylase	rice actin		PMON78918
549	PHE0001233	1323	rice G1073-like 1	rice actin		
550	PHE0001234	1324	rice inosine monophosphate dehydrogenase - AAK09225	rice actin		PMON81788
551	PHE0001235	1325	yeast IMP dehydrogenase [Imd2p] - NP_012088	rice actin		PMON78945
552	PHE0001236	1326	E. coli guaB - NP_417003	rice actin		PMON78946
553	PHE0001237	1327	Agrobacterium GuaB - AE007996	rice actin		PMON80288
554	PHE0001276	1366	corn Transcription Factor #1	rice actin		PMON79652
555	PHE0001277	1367	corn Transcription Factor #2	rice actin		PMON75519
556	PHE0001325	591	corn RING finger protein 25	rice actin		PMON69495
557	PHE0001326	1416	yeast VHT1 - YGR065C	rice actin		PMON75961
557	PHE0001326	1417	yeast VHT1 - YGR065C	rice actin	chloroplast	
558	PHE0001327	1418	Arabidopsis Suc5 - AJ252133	rice actin		
559	PHE0001400	1492	soy G1792-like 2	rice actin		PMON75500
560	PHE0001401	1493	corn G1792-like 3	rice actin		PMON80907
561	PHE0001423	1515	Glutamate Decarboxylase	rice actin		PMON79672
562	PHE0001432	1524	putative carnitine/acylcarnitine translocase-	rice actin		
563	PHE0001433	1525	corn cycA-like [GATE80]	rice actin		
564	PHE0001434	1526	corn cycA-like [GAT81]	rice actin		
565	PHE0001435	1527	corn E4/E8 binding protein-like [GATE68]	rice actin		
566	PHE0001438	1530	Arabidopsis G748	rice actin		PMON81202
567	PHE0001439	1531	Arabidopsis NAM (no apical meristem)-like protein-	rice actin		
568	PHE0001440	1532	soy G1452-like protein	rice actin		PMON79165
569	PHE0001497	1588	corn cytochrome P450	rice actin		PMON79674
570	PHE0001498	1589	rice receptor-like protein	rice actin		
571	PHE0001499	1590	rice receptor-like protein kinase	rice actin		
572	PHE0001500	1591	rice putative brassinosteroid-insensitive protein	rice actin		
573	PHE0001501	1592	rice cell elongation protein DIMINUTO	rice actin		
574	PHE0001502	1593	corn Dwarf1-like 1	rice actin		PMON80908
575	PHE0001503	1594	rice putative sterol-C5(6)-desaturase	rice actin		
576	PHE0001504	1595	corn sterol-C5(6)-desaturase 2	rice actin		PMON75535
577	PHE0001505	1596	corn sterol-C5(6)-desaturase 1	rice actin		PMON75536
578	PHE0001506	1597	soy sterol-C5(6)-desaturase	rice actin		PMON75537
579	PHE0001507	1598	rice BRS1-like protease 4	rice actin		PMON81761
580	PHE0001508	1599	corn BRS1-like protease 1	rice actin		

SEQ ID NO	Phe ID	Nom ID	Gene Name	Promoter	Target	pMON
581	PHE0001509	1600	soy FKF1-like protein	rice actin		PMON75540
582	PHE0001510	1601	corn FKF-like protein 2	rice actin		
583	PHE0001542	1633	yeast YDL168W/SFA1 - NP_010113	rice actin		PMON79183
584	PHE0001543	1634	E. coli adhC - AE000142	rice actin		
585	PHE0001544	1635	Nostoc sp. PCC 7120 glutathione dependent formaldehyde dehydrogenase-BAB74509	rice actin		
586	PHE0001545	1636	rice glutathione dependent formaldehyde dehydrogenase-U77637	rice actin		PMON80543
587	PHE0001546	1637	corn glutathione-dependent formaldehyde dehydrogenase-Y11029	rice actin		PMON79717
588	PHE0001547	1638	corn corn glutathione-dependent formaldehyde dehydrogenase 2-	rice actin		PMON79184
589	PHE0001548	1639	corn corn glutathione-dependent formaldehyde dehydrogenase 3-	rice actin		PMON75547
590	PHE0001549	1640	soy glutathione dependent formaldehyde dehydrogenase-	rice actin		PMON79185
591	PHE0001550	1641	rice putative phosphate translocator - AAK21346	rice actin		PMON82206
592	PHE0001551	1642	rice glucose-6-phosphate/phosphate-tranlocator-13486660	rice actin		
593	PHE0001552	1643	corn glucose-6-phosphate/phosphate-tranlocator-	rice actin		PMON79186
594	PHE0001553	1644	rice putative sugar transporter - AF416867	rice actin		
595	PHE0001554	1645	soy cycD4-like protein	rice actin		PMON79187
596	PHE0001578	1677	rice RPN12 - AB037153	rice actin		
597	PHE0001579	1678	YFR052W/RPN12 - NP_116710	rice actin		PMON79189
598	PHE0001580	1679	corn rpn12	rice actin		PMON79190
599	PHE0001581	1680	soy rpn12	rice actin		PMON79191
600	PHE0001583	1682	sorghum TTG1-like	rice actin		PMON82185
601	PHE0001584	1683	corn TTG1-like protein 2	rice actin		
602	PHE0001595	1702	ZmHK1	rice actin		
603	PHE0001596	1704	Arabidopsis CRE1b	rice actin		
604	PHE0001597	1706	Arabidopsis HK2	rice actin		
605	PHE0001598	1708	Arabidopsis HK3	rice actin		
606	PHE0001607	1718	maize nitrate transporter like 1 sequence	rice actin		
607	PHE0001608	1719	rice nitrate transporter like 1 sequence	rice actin		
608	PHE0001609	1720	rice nitrate transporter like 2 sequence	rice actin		
609	PHE0001667	1778	rice histidine kinase	rice actin		
610	PHE0002018	2129	Arabidopsis nitrate transporter NTL1 like sequence	rice actin		PMON79677
611	PHE0002019	2130	maize nitrate transporter NTL1	rice actin		PMON82187

SEQ ID NO	Phe ID	Nom ID	Gene Name	Promoter	Target	pMON
			like sequence			
612	PHE0002020	2131	maize nitrate transporter NTL1 like 2 sequence	rice actin		PMON82208
613	PHE0002021	2132	rice nitrate transporter NTL1 like 1 sequence	rice actin		PMON80309
614	PHE0002022	2133	rice nitrate transporter NTL1 like 2 sequence	rice actin		PMON81291

Example 2 Constructs for Soybean Transformation

Constructs for use in transformation of soybean may be prepared by restriction enzyme based cloning into a common expression vector. Elements of an exemplary common expression vector are shown in Table 7 below.

TABLE 7 Elements of pMON74532

Function	Element	Reference
Agro transformation	B-ARGtu.right border	Depicker, A. et al (1982) Mol Appl Genet 1:561-573
Antibiotic resistance	CR-Ec.aadA-SPC/STR	
Repressor of primers from the ColE1 plasmid	CR-Ec.rop	
Origin of replication	OR-Ec.oriV-RK2	
Agro transformation	B-ARGtu.left border	Barker, R.F. et al (1983) Plant Mol Biol 2:335-350
Plant selectable marker expression cassette	Promoter with intron and 5'UTR of arabidopsis act 7 gene (AtAct7)	McDowell *et al.* (1996) Plant Physiol. 111:699-711.
	5' UTR of arabidopsis act 7 gene	
	Intron in 5'UTR of AtAct7	
	Transit peptide region of Arabidopsis EPSPS	Klee, H.J. *et al* (1987) MGG 210:437-442
	Synthetic CP4 coding region with dicot preferred codon usage	U.S. Patent 6,248,876
	A 3' UTR of the nopaline synthase gene of Agrobacterium tumefaciens Ti plasmid	U.S. Patent 5,858,742

Plant gene of interest expression cassette	Promoter for 35S RNA from CaMV containing a duplication of the -90 to -350 region	U.S. Patent 5,322,938
	Gene of interest insertion site	
	Cotton E6 3' end	GenBank accession U30508

Vectors similar to that described above may be constructed for use in *Agrobacterium* mediated soybean transformation systems where the enhanced 35S promoter in the plant expression cassette portion is replaced with other desirable promoters including, but not limited to a napin promoter and an *Arabidopsis* SSU promoter. Protein coding segments are amplified by PCR prior to insertion into vectors such as described above. Primers for PCR amplification can be designed at or near the start and stop codons of the coding sequence, in order to eliminate most of the 5’ and 3’ untranslated regions.

Exemplary sense constructs for transformation of soybean to produce plants having enhanced phenotypes are provided in Table 8 below.

“SEQ ID NO” refers to a particular nucleic acid sequence in the Sequence Listing which defines a polynucleotide used in a recombinant polynucleotide of this invention.
“PHE ID” refers to an arbitrary number used to identify a particular recombinant polynucleotide corresponding to the translated protein encoded by the polynucleotide.
“NOM ID” refers to a particular construct comprising a polynucleotide of this invention.
“GENE NAME” refers to a common name for the recombinant polynucleotide.
“PROMOTER” provides the name of the promoter region driving expression of the polynucleotide
“pMON” refers to an arbitrary number used to designate a particular recombinant DNA construct. Constructs are prophetic where no pMON is provided.
“Gene effect contributing to increased yield” describes the effect of the recombinant polynucleotide on the plant in providing yield improvement.

TABLE 8 Soybean Transformation Constructs

SEQ ID NO	Phe ID	Nom ID	Gene Name	Promoter	pMON	Gene effect contributing to increased yield
3	PHE0000004	4018	corn AtHAP3a-like2	e35S		Enhanced water use efficiency
9	PHE0000080	3442	G28/BAA32418	e35S	PMON81704	Enhanced fungal resistance
22	PHE0000372	3649	G1073	napin	PMON81727	Enhanced plant growth and development
23	PHE0000373	3437	G1411	e35S	PMON81802	Improved light capture
24	PHE0000374	3650	G1449	e35S	PMON81760	Improved light capture
220	PHE0000655	3436	G1435	e35S	PMON81705	Increased leaf mass and photosynthetic rate
222	PHE0000658	3652	G1496	e35S	PMON81768	Enhanced plant morphology and development
229	PHE0000666	3576	Brassica P-II	e35S	PMON81730	Enhanced nitrogen use efficiency
254	PHE0000743	3966	yeast DBF2 - P22204	e35S		Cold tolerant germination and seedling growth
256	PHE0000745	3440	Arabidopsis agl8 - Q38876	e35S	PMON81757	Enhanced plant growth and development
281	PHE0000779	3434	yeast GPA2	e35S	PMON81729	Seedling cold vigor
286	PHE0000800	3946	AtSUC1	e35S		Increased sucrose transport/production Increased photosynthesis
286	PHE0000800	3947	AtSUC1	AtSSU1A		Increased sucrose transport/production Increased photosynthesis
287	PHE0000801	3948	Arabidopsis SUT2	e35S		Increased sucrose transport/production Increased photosynthesis
287	PHE0000801	3949	Arabidopsis SUT2	AtSSU1A		Increased sucrose transport/production Increased photosynthesis
291	PHE0000805	3950	Aspergillis phytochrome	e35S		Enhanced plant growth and development
302	PHE0000816	3441	G1792	e35S	PMON81830	Enhanced fungal resistance
524	PHE0001044	3647	soy AGL8-like 1	e35S	PMON81-713	Enhanced plant growth and development

Example 3 Plant Transformation

Maize Transformation

LH59 plants are grown in the greenhouse and ears and ears harvested. when the embryos are 1.5 to 2.0 mm in length. Ears were surface sterilized by spraying or soaking the ears in 80% ethanol, followed by air drying. Immature embryos were isolated from individual kernels on surface sterilized ears. Prior to inoculation of maize cells, *Agrobacterium* cells are grown overnight at room temperature. Immature maize embryos are inoculated with *Agrobacterium* shortly after excision, and incubated at room temperature with *Agrobacterium* for 5-20 minutes. Immature embryos are then co-cultured with *Agrobacterium* for 1 to 3 days at 23°C in the dark. Co-cultured embryos are transferred to selection media and cultured for approximately two weeks to allow embryogenic callus to develop. Embryogenic callus is transferred to culture medium containing 100 mg/L paromomycin and subcultured at about two week intervals. Transformants are recovered 6 to 8 weeks after initiation of selection.

For *Agrobacterium* mediated transformation of maize callus, immature embryos are cultured for approximately 8-21 days after excision to allow callus to develop. Callus is then incubated for about 30 minutes at room temperature with the *Agrobacterium* suspension, followed by removal of the liquid by aspiration. The callus and *Agrobacterium* are co-cultured without selection for 3-6 days followed by selection on paromomycin for approximately 6 weeks, with biweekly transfers to fresh media, and paromomycin resistant callus identified.

For transformation by microprojectile bombardment, immature maize embryos are isolated and cultured 3-4 days prior to bombardment. Prior to microprojectile bombardment, a suspension of gold particles is prepared onto which the desired DNA is precipitated. DNA is introduced into maize cells as described in U.S. Patent No. 5,015,580 using the electric discharge particle acceleration gene delivery device. For microprojectile bombardment of LH59 pre-cultured immature embryos, 35% to 45% of maximum voltage is preferably used. Following microprojectile bombardment, tissue is cultured in the dark at 27°C.

Fertile transgenic plants are produced from transformed maize cells by transfer of. transformed callus to appropriate regeneration media to initiate shoot development. Plantlets are transferred to soil when they are about 3 inches tall and have roots (about four to 6 weeks after transfer to medium). Plants are maintained for two weeks in a growth chamber at 26°C, followed by two weeks on a mist bench in a greenhouse before transplanting to 5 gallon pots for greenhouse growth. Plants are grown in the greenhouse to maturity and reciprocal pollinations made with the inbred LH59. Seed is collected from plants and used for further breeding activities.

Transformation methods and materials for making transgenic plants of this invention, e.g. various media and recipient target cells, transformation of immature embryos and subsequent regeneration of fertile transgenic plants are disclosed in U.S. Patents 6,194,636 and 6,232,526 and U.S. patent application Serial No. 09/757,089, which are incorporated herein by reference.

Soybean Transformation

For *Agrobacterium* mediated transformation, soybean seeds are germinated overnight and the meristem explants excised. The meristems and the explants are placed in a wounding vessel. Soybean explants and induced *Agrobacterium* cells from a strain containing plasmid DNA with the gene of interest cassette and a plant selectable marker cassette are mixed no later than 14 hours from the time of initiation of seed germination and wounded using sonication. Following wounding, explants are placed in co-culture for 2-5 days at which point they are transferred to selection media for 6-8 weeks to allow selection and growth of transgenic shoots. Phenotype positive shoots are harvested approximately 6-8 weeks post bombardment and placed into selective rooting media for 2-3 weeks. Shoots producing roots are transferred to the greenhouse and potted in soil. Shoots that remain healthy on selection, but do not produce roots are transferred to non-selective rooting media for an additional two weeks. Roots from any shoots that produce roots off selection are tested for expression of the plant selectable marker before they are transferred to the greenhouse and potted in soil.

Descriptions of media useful for transformation and regeneration of soybean and a method employing microprojectile bombardment are described in US patent 5,914,451, which is incorporated herein by reference.

Example 4 Identification of Homologs

A BLAST searchable "All Protein Database" was constructed of known protein sequences using a proprietary sequence database and the National Center for Biotechnology Information (NCBI) non-redundant amino acid database (nr.aa). For each organism from which a polynucleotide sequence provided herein was obtained, an "Organism Protein Database" was constructed of known protein sequences of the organism; it is a subset of the All Protein Database based on the NCBI taxonomy ID for the organism.

The All Protein Database was queried using each of the polypeptide sequences of SEQ ID NO:615 through SEQ ID NO:1228 using "blastp" with E-value cutoff of 1e-8. Up to 1000 top hits were kept, and separated by organism names. For each organism other than that of the query sequence, a list was kept for hits from the query organism itself with a more significant E-value than the best hit of the organism. The list contains likely duplicated genes of the polynucleotides provided herein, and is referred to as the Core List. Another list was kept for all the hits from each organism, sorted by E-value, and referred to as the Hit List.

The Organism Protein Database was queried using polypeptide sequences of SEQ ID NO:615 through SEQ ID NO:1228 using "blastp" with E-value cutoff of 1e-4. Up to 1000 top hits were kept. A BLAST searchable database was constructed based on these hits, and is referred to as "SubDB". SubDB was queried with each sequence in the Hit List using "blastp" with E-value cutoff of 1e-8. The hit with the best E-value was compared with the Core List from the corresponding organism. The hit is deemed a likely ortholog if it belongs to the Core List, otherwise it is deemed not a likely oththolog and there is no further search of sequences in the Hit List for the same organism. Likely orthologs from a large number of distinct organisms were identified and are reported by amino acid sequences of SEQ ID NO:1229 to SEQ ID NO: 27373. These orthologs are reported in Table 1 as homologs to the 614 polypeptides provided herein. The contensts of Table 1 are illustrated in the Abbreviated Table 1 which lists the othrologs sequences for the polypeptide sequences of SEQ ID NO:615 and 616.

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                        Abbreviated Table 1
615:25857 8201 19323 26202 14281 14995 22777 21309 26139 22368 20627 22283
     8339 13615 25432 22091 22905 23419 9135 11938 8903 13509 21851 23709
     12432 13984 12136 7610 26380 22940 7611 11937 7104 7609 8859 24920
     7109 21186 22098
616:14995 22777 21309 26139 22368 20627 9778 9694 18287 2667 2565 1944
     1636 2666 2251 2087 15823 22303 4448 8339 13615 25432 22091 22905
     23419 9135 11938 13509 21851 23709 12432 13984 18015 12136 11937
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Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claims.